

Biology 18

Neuchâtel, 14-16 February

unine

UNIVERSITÉ DE
NEUCHÂTEL



MUSÉUM
D'HISTOIRE NATURELLE
NEUCHÂTEL



Swiss Zoological Society



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Swiss Institute of
Bioinformatics



frontiers in Ecology and Evolution



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Acknowledgements

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Daniel Croll and Sergio Rasmann

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Plenary speakers

Anna-Liisa Laine, Anna-Sapfo Malaspinas, Raphaël Arlettaz, and Klaus Zuberbühler.

Volunteers

Célia Ruiz, Fanny Kupferschmid, Yann Jeanneret, Marika de Fabritiis, Camile Kessler, Charlotte Bellot, Merlin Gay, Eric Nabil Risse, Leen Abraham, Yasmin Emery, Juan Trainee, Alba Hendier, Caroline Gaille, Hakim Schepis, Sarah Semeraro, and Veronica Caggia.

Darwin Dinner

Darwin Lecture by Nicolas Perrin.

Catering Service: Cinq-Sens, Wodey-Suchard SA.

Music Band: Cocinado, DJ: Jonas Durand & Romain Bessire.

Scientific speed-dating

Tania Jenkins, Zegni Triki, Jessica Litman, Igor Chlebyn

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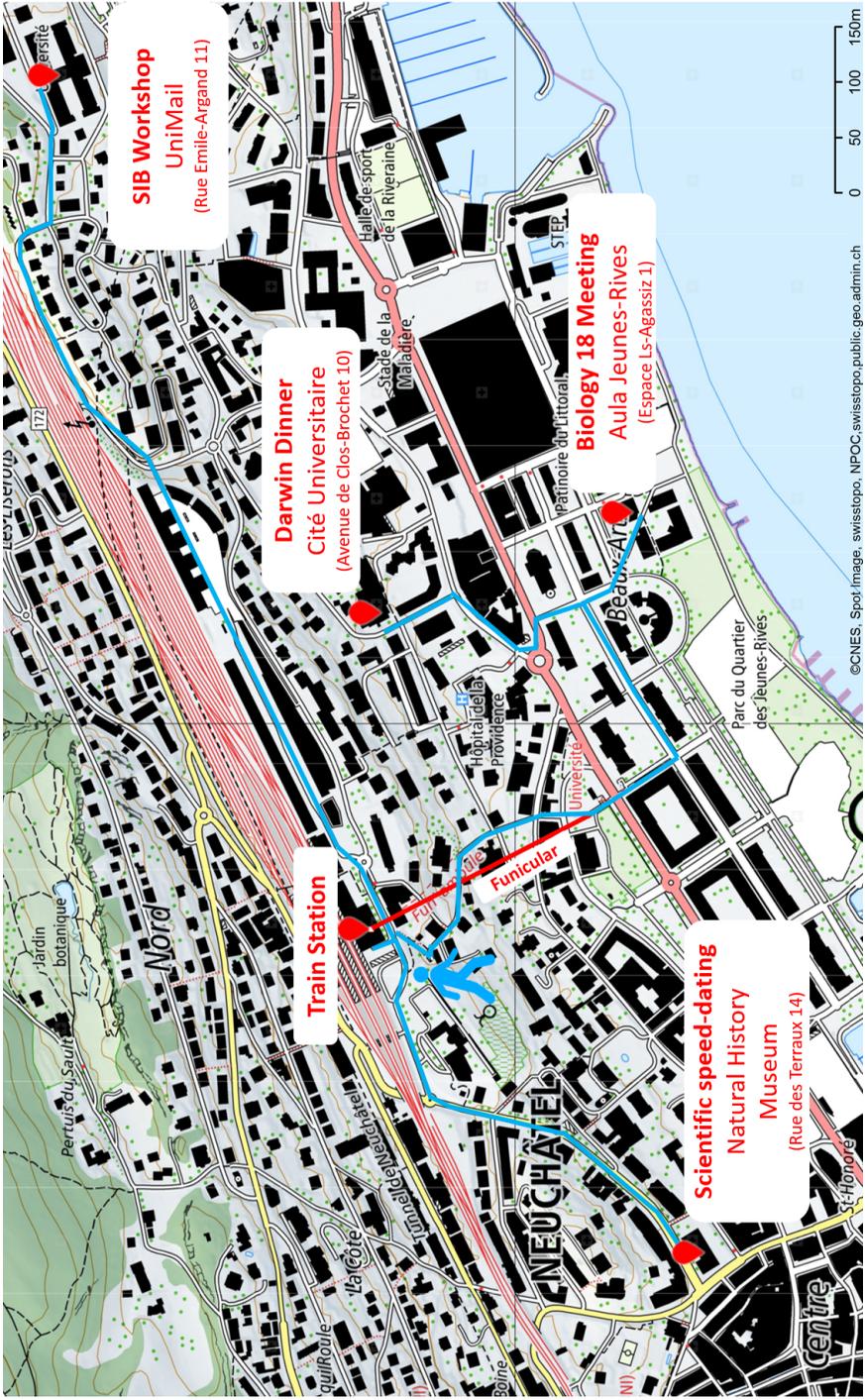
Jardin botanique de Neuchâtel

Caves de la Ville de Neuchâtel

Hôtel des Arts

Migros

Frontiers



Train Station

Scientific speed-dating
Natural History Museum
(Rue des Terraux 14)

Darwin Dinner
Cité Universitaire
(Avenue de Clos-Brochet 10)

Biology 18 Meeting
Aula Jeunes-Rives
(Espace Ls-Agassiz 1)

SIB Workshop
UniMail
(Rue Emile-Argand 11)

Funicular

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0 50 100 150m

General Information

Emergencies on campus

Ambulance: 114, Fire Fighters: 118, Police: 117. For any minor incidents please contact either Michel Neier (tel. 032 718 27 81) or Roxanne Kohler (tel. 032 718 27 80).

Conference venue

The main conference will take place at the Aula Jeunes-Rives (see map). Parallel sessions will be held at the Aula, and rooms RN.02 and RE.48. Poster sessions will be held at the entrance of the three rooms.

Information and registration desk

The information desk is located at the entrance of the venue at Aula Jeunes-Rives and will be staffed throughout the main conference.

WiFi

The **eduroam** network will provide anyone with internet connectivity. Use your username@university_domain.ch and corresponding password to log in.

Lunch and coffee breaks

For those who purchased lunch vouchers, lunch is available at the main entrance of the Aula Jeunes-Rives. Coffee breaks are also held at the same place.

Travel and public transport

The SBB-CFF Neuchâtel train station can easily be reached from any city in Switzerland. Timetables and tickets are available at <http://sbb.ch/en>. In Neuchatel, public transport information is offered by Onde Verte (<http://ondeverte.ch>). Taking the funicular from the train station down to the conference site requires a separate ticket.

Accessibility

Please contact us in advance if you have any accessibility needs and we are happy to provide assistance.

Information for presenters

Talks - Please upload your presentation 30 min before your session at the registration desk. For oral presentations, files should be .pdf or .pptx. Talks should not take longer than 12 min plus 3 min of questions. Flash talks should be a single slide (animations are possible) and not longer than 2 min. Please respect these length restrictions.

Posters (standard A0 portrait format) - Two separate poster sessions are held on Thursday and Friday. Please hang your poster in the morning before the plenary talk on the boards matching your number (available in the abstract book and at the registration desk). Please remove your poster by the end of the day to free the board for the next poster session.

Detailed Conference Program

Wednesday 14.2 – SIB Workshop

	Auditorium Louis-Guillaume (UniMail – 2nd floor)
13:45 – 14:00	REGISTRATION AND WELCOME
	SWISS INSTITUTE OF BIOINFORMATICS WORKSHOP Chair: ALAN KERGUNTEUIL
14:00 – 14:20	PATRICIA PALAGI – SIB
	Introduction to computational biology and the Swiss Institute of Bioinformatics
14:20– 15:05	FRÉDÉRIC BASTIAN – U. LAUSANNE, SIB
	Bgee: gene expression evolution bioinformatics
15:05 – 15:50	VIVIAN LINK – U. FRIBOURG, SIB
	Go low with ATLAS: a tool for maximizing insight from minimal sequencing depth
15:50 – 16:20	COFFEE BREAK
16:20 – 17:05	MASSIMO MAIOLO – ZHAW, SIB
	Fast and accurate reconstruction of multiple sequence alignments using an evolutionary indel model
17:05 – 17:30	GENERAL DISCUSSION
18:00 – 20:45	SCIENTIFIC SPEED-DATING WELCOME APÉRO (NATURAL HISTORY MUSEUM OF NEUCHÂTEL)

Thursday 15.2 (morning)

	Aula – JEUNES-RIVES
8:15	REGISTRATION DESK OPEN
8:40 – 8:45	WELCOME AND OPENING REMARKS
8:45 – 9:30	ANNA-LIISA LAINE – U HELSINKI
	Uncovering diversity and its drivers in a large natural pathogen metapopulation
Session	EVOLUTIONARY GENETICS CHAIR: EMILIE CHANCLUD
9:30 – 9:45	GIACOMO ZILIO – U. NEUCHATEL
	The effect of parasite infection on the recombination rate of the yellow fever mosquito <i>Aedes aegyti</i>
9:45 – 10:00	ANA PAULA MACHADO – U. LAUSANNE
	The Rocky Mountains as a dispersal barrier between barn owl (<i>Tyto alba</i>) populations in North America
10:00 – 10:15	JAN-NIKLAS RUNGE – U. ZURICH
	Selfish manipulation of migration propensity in house mice
10:15 – 10:30	URSULA OGGENFUSS – U. NEUCHATEL
	A population-level invasion by transposable elements in a fungal pathogen
10:30 – 11:00	COFFEE BREAK
Session	SEX AND LIFE HISTORY CHAIR: ALFONSO ROJAS
11:00 – 11:15	XIANG-YI LI – U. ZURICH
	Can sexual dimorphism evolve because of natural selection?
11:15 – 11:30	PATRICK JOYE – U. LAUSANNE
	How is female mating choice impacted by presence of pathogens?
11:30 – 11:45	SAKSHI SHARDA – EPFL
	There's a predator around, run! Maternal effects through eggs affect offspring growth and anti-predator responses
11:45 – 12:00	CINDY DUPUIS – U. LAUSANNE
	Adaptation to juvenile malnutrition: Trade-off with adult performances
12:00 – 12:20	POSTER FLASH TALKS
	DIOGO ANTUNES – U. BERN; MATTHEW BARBOUR – U. ZURICH ATHIMED EL TAHER – U. BASEL; YAËLLE BOUQUET – U. NEUCHATEL
12:20 – 14:15	LUNCH BREAK AND POSTER SESSION (SZS MEETING AT 13:00)

Thursday 15.2 (morning)

RN.02 and video link to RE.48 – JEUNES-RIVES	
Session	BIOTIC INTERACTIONS CHAIR: ADRIENNE GODSCHALX
9:30 – 9:45	ANNE KEMPEL - SWEDISH UNIVERSITY OF AGRIC. SCIENCES UMEA Local adaptation of plant-herbivore interactions along a soil fertility gradient
9:45 – 10:00	DANIEL SCHLÄPPI – U. BERN Virus spillover from European honey bees (<i>Apis mellifera</i>) to ants (<i>Lasius niger</i>)
10:00 – 10:15	PETTERI KARISTO – ETH ZURICH Two types of resistance against a major wheat disease Septoria tritici Blotch
10:15 – 10:30	DOLORES GENNÉ VIZCARDO – U. NEUCHATEL Competition of two <i>Borrelia</i> strains inside the rodent host and the tick vector
10:30 – 11:00	COFFEE BREAK
Session	CHEMISTRY AND INTERACTION CHAIR: MOJTABA MOKHTIARI
11:00 – 11:15	ADRIN DÜRST – U. ZURICH Another one bites the leaf: Heterophylly of Mascarene plants as an adaptation to giant tortoise herbivory
11:15 – 11:30	CORINNE HERTAEG – ETH ZURICH Wasps with a chemical invisibility cloak
11:30 – 11:45	ADRIENNE GODSCHALX – U. NEUCHATEL Floral volatiles and corresponding transcript expression of brood-site mimic, <i>Arum maculatum</i> , are geographically structured and vary according to the dominant pollinator species
11:45 – 12:00	PHILLIPE PICCARDI – U. LAUSANNE A small microbial community for the degradation of a pollutant
12:00 – 12:20	POSTER FLASH TALKS CHRISTOPHE PRAZ – U. NEUCHATEL; THOMAS GOEURY– U. GENEVA MAX SCHMID – U. ZURICH; CLAUDIO SEBASTIÁN QUILODRÁN VENEGAS – U. OXFORD, U. GENEVA
12:20 – 14:15	LUNCH BREAK AND POSTER SESSION

Thursday 15.2 (afternoon)

	Aula – JEUNES-RIVES
14:15-15:00	KLAUS ZUBERBÜHLER – U NEUCHATEL
	The ethology of primate cognition
Session	BEHAVIOUR CHAIR: ZEGNI TRIKI
15:00 – 15:15	LORENZO ARDUINI – U. BERN
	Awareness of danger in cuttlefish embryo
15:15 – 15:30	MUTKA WATVE – U. BERN
	When in doubt, observe your parents!
15:30 – 15:45	CLAUDIA KASPER – U. BERN
	Divergent brain gene expression profiles between alternative behavioural helper types in a cooperative breeder
15:45 – 16:00	STÉPHANIE MERCIER – U. NEUCHATEL
	Wild vervet monkey screams inform potential helpers on caller's social role and conflict severity
16:00 – 16:30	COFFEE BREAK AND POSTER SESSION
Session	COOPERATION CHAIR: ALAN KERGUNTEUIL
16:30 – 16:45	RAMONA RAUBER – U. ZURICH
	Too hungry to cooperate: influence of drought on sentinel behaviour and its vocal coordination in meerkats
16:45 – 17:00	JAN NAEF – U. BERN
	Trading of different commodities in a cooperatively breeding fish
17:00 – 17:15	JENNIFER MCCLUNG – U. NEUCHATEL
	Variation in human cooperation: Key proximate mechanisms
17:15 – 17:30	JON ANDREJA NOUTCLÀ – U. BERN
	How ambrosia beetles predict the weather and what this can teach us about the evolution of cooperation
18:00 – 24:00	DARWIN DINNER AT CITÉ UNIVERSITAIRE 18:00 APÉRO 18:30 TALK BY NICOLAS PERRIN (A BRIEF HISTORY OF SEXES) 19:30 DINNER AND PARTY

Thursday 15.2 (afternoon)

	RN.02 and video broadcast on RE.48 – JEUNES-RIVES
Session	ECOLOGY AND LIFE HISTORY TRAITS CHAIR: ALFONSO ROJAS
15:00 – 15:15	NINO MAAG – U. ZURICH
	Density-dependent dispersal strategies in a cooperative breeder
15:15 – 15:30	PHILLIP DERMOND – U. BERN, EAWAG
	Tradeoffs between predation and growth determine differential migration
15:30 – 15:45	SONIA LÖTSCHER – U. ZURICH
	Environmental and anthropogenic determinants of the structure of Alpine marmot family groups
15:45 – 16:00	SAMANTHA V. BECK – U. ICELAND
	Maternal effects and early developmental changes in gene expression in polymorphic Arctic charr (<i>Salvelinus alpinus</i>)
16:00 – 16:30	COFFEE BREAK AND POSTER SESSION
Session	SYSTEMATICS AND MACROEVOLUTION CHAIR: CHRISTOPHE PRAZ
16:30 – 16:45	JESSICA LITMAN – NATURAL HISTORY MUSEUM NEUCHATEL
	A DNA barcode library for Swiss diurnal Lepidoptera: Implications for species identification, systematics and conservation
16:45 – 17:00	TRISTAN CORDIER – U. GENEVA
	High-throughput biomonitoring of marine ecosystems with eDNA: supervised machine learning for the building of robust predictive models.
17:00 – 17:15	MARIO COIRO – U. ZURICH
	Untangling diversity and disparity in the macroevolutionary history of the cycadales
17:15 – 17:30	SIB TALK BY PABLO DUCHEN – U. LAUSANNE
	The role of migration in speciation: linking micro- and macro-evolution

Friday 16.2 (morning)

	Aula – JEUNES-RIVES
8:45 - 9:30	ANNA-SAPFO MALASPINAS – U. LAUSANNE
	A genomic perspective of the peopling of the first (Australia) and the last (the Americas) continents being colonized by humans
Session	ADAPTATION AND GENOMICS CHAIR: EMILIE CHANCLUD
9:30 – 9:45	DIANA IVETTE CRUZ-DAVALOS – U. BERN, U. LAUSANNE
	Genomics of ancient Brazilian populations
9:45 – 10:00	NORA HOHMANN – U. BASEL
	Parallel adaptation to climate in quaternary lineages of North American <i>Arabidopsis lyrata</i>
10:00 – 10:15	JOANA MEIER – U. BERN
	The reticulate evolution of Lake Victoria cichlids
10:15 – 10:30	SOPHIE ARCHAMBEAULT – U. BERN, U. WASHINGTON
	The architecture of adaptation: a mass of mutations or a master mutation?
10:30 – 11:00	COFFEE BREAK
Session	ADAPTATION AND GENOMICS CHAIR: ALFONSO ROJAS
11:00 – 11:15	LUZIA STALDER – U. NEUCHATEL, ETH ZURICH
	Recent adaptive evolution through segmental duplications in a semi-clonal fungal pathogen
11:15 – 11:30	EVA KOCH – U. ZURICH
	Combining transcriptomic and fitness data to study plastic and evolved responses to environmental changes
11:30 – 11:45	CAS RETEL – U. BERN, EAWAG
	Genomics of host-virus coevolution
11:45 – 12:00	CAMILLE AMELINE – U. BASEL
	Genetics of parasite resistance in a co-evolving population
12:00 – 12:20	POSTER FLASH TALKS
	YASEMIN KURTOGULLARI – U. BERN; MARCO MORETTI - WSL RAPHAELA HEESEN – U. NEUCHATEL; LUKAS WIDMER – U. BASEL
12:20 – 14:15	LUNCH BREAK AND POSTER SESSION

Friday 16.2 (morning)

	RN.02 and video broadcast on RE.48 – JEUNES-RIVES
Session	ECOSYSTEMS CHAIR: MOJTABA MOKHTIARI
9:30 – 9:45	NOÉMIE PICHON – U. BERN
	The PaNDiv Experiment: individual and interactive effects of diversity, functional composition and nitrogen on grassland ecosystem functioning
9:45 – 10:00	FRANK PENNEKAMP – U. ZURICH
	Biodiversity increases and decreases ecosystem stability
10:00 – 10:15	SOFIA VAN MOORSEL – U. ZURICH
	Community evolution increases the stability of grassland plant communities during unperturbed and perturbed states
10:15 – 10:30	MALTE JOCHUM – U. BERN
	Are the plant communities of biodiversity experiments representative of naturally assembled ecosystems?
10:30 – 11:00	COFFEE BREAK
Session	ECOLOGY AND SPECIATION CHAIR: ADRIENNE GODSCHALX
11:00 – 11:15	SIMONE FONTANA - WSL
	Niche partitioning among individuals in natural phytoplankton communities and experimental populations
11:15 – 11:30	CARMELA DOENZ – U. BERN, EAWAG
	Ecological opportunity predicts charr diversity of Greenlandic lakes
11:30 – 11:45	SACHA ZAHND – U. LAUSANNE
	Ecological predictors of social organization in the Alpine silver ant
11:45 – 12:00	ANAÏS TILQUIN – U. ZURICH
	Endosymbiosis, the original sin? How cell fusion could have evolved to mitigate mitochondrial meltdown
12:00 – 12:20	POSTER FLASH TALKS
	NIKOLETA ANICIC – U. ZURICH; DAVID DREIFUSS – U. GENEVA PAMELA BRUNO – U. NEUCHATEL; DAMIAN ORTIZ RODRIGUEZ – ETH/WSL
12:20 – 14:15	LUNCH BREAK AND POSTER SESSION

Friday 16.2 (afternoon)

	Aula – JEUNES-RIVES
14:15 - 15:00	RAPHAËL ARLETTAZ – U. BERN
	The 6th (mass) extinction: research for action
Session	POPULATION GENETICS CHAIR: ANDREA GOMEZ CHAMORRO
15:00 – 15:15	CHARLES MULLON – U. LAUSANNE
	Social polymorphism is favoured by the co-evolution of dispersal with social behaviour
15:15 – 15:30	LUIZ JARDIM DE QUEIROZ – U. GENEVA
	Origin of genetic diversity in an Amazonian fish and how to belong to a same population despite being separated by a strong environmental barrier
15:30 – 15:45	MARCO GALIMBERTI – U. FRIBOURG
	Detecting selection from linked sites using an F-model
15:45 – 16:00	KIMBERLY GILBERT – U. BERN
	The dynamics of expansion load and recovery during species range shifts
16:00 – 16:15	CHAMPAK BEERAVOLU REDDY – U. ZURICH
	Blockwise site frequency spectra for inferring complex population histories and recombination
16:15 – 16:45	COFFEE BREAK AND POSTER SESSION
16:45 – 17:00	AWARD CEREMONY AND CLOSING

Friday 16.2 (afternoon)

	RN.02 and video broadcast on RE.48 – JEUNES-RIVES
Session	CONSERVATION CHAIR: BETTY BENREY
15:00 – 15:15	LAURA BOSCO – U. BERN
	Effects of habitat quality and fragmentation on Woodlarks (<i>Lullula arborea</i>) and their invertebrate prey in intensively managed vineyards
15:15 – 15:30	LUCA GAGGINI – U. BASEL
	The invasive plant <i>Impatiens glandulifera</i> affects soil fungal diversity and the bacterial community in forests
15:30 – 15:45	OLIVIA RUSCONI – U. NEUCHATEL
	Conservation of endangered plants: a roadmap for the selection of translocation sites
15:45 – 16:00	OLIVIER DOSCH – U. ZURICH
	Terrestrial habitat fragmentation determines abundance of aquatic salamander larvae
16:00 – 16:15	CHANTAL HERZOG – AGROSCOPE
	Consequences of long-term organic farming on yield and environmental performance
16:15 – 16:45	COFFEE BREAK AND POSTER SESSION

Wednesday 14.2	Thursday 15.2	Friday 16.2		
	8:15 Registration 8:40 Welcome remarks	8:15 Registration		
	8:45 – 9:30 Plenary by Anna-Liisa Laine U Helsinki	8:45 – 9:30 Plenary by Anna-Sapfo Malaspinas U Lausanne		
	9:30 – 10:30 Evolutionary Genetics	9:30 – 10:30 Biotic Interactions	9:30 – 10:30 Adaptation and Genomics	9:30 – 10:30 Ecosystems
	10:30 – 11:00 Coffee Break	10:30 – 11:00 Coffee Break		
	11:00 – 12:00 Sex and Life History	11:00 – 12:00 Chemistry and Interaction	11:00 – 12:00 Adaptation and Genomics	11:00 – 12:00 Ecology and Speciation
	12:00 – 12:20 Poster Flash Presentations	12:00 – 12:20 Poster Flash Presentations		
SIB Swiss Institute of Bioinformatics - Workshop	12:20 – 14:15 Lunch Poster session	12:20 – 14:15 Lunch Poster session		
13:45 Registration / Welcome	14:15 – 15:00 Plenary by Klaus Zuberbühler U Neuchâtel	14:15 – 15:00 Plenary by Raphaël Arlettaz U Bern		
14:00–15:45 Talks	15:00 – 16:00 Behaviour	15:00 – 16:00 Ecology and Life History Traits	15:00 – 16:00 Population Genetics	15:00 – 16:00 Conservation
15:45 – 16:15 Coffee Break	16:00 – 16:30 Coffee & Poster Session	16:15 – 16:45 Coffee & Poster Session		
16:15–17:00 Talk	16:30 – 17:30 Cooperation	16:30 – 17:30 Systematics and Macroevolution	16:45 – 17:00 Award ceremony & closing	
17:00–17:30 Discussion				
Scientific Speed- Dating (Natural History Museum) 18:00 - 20:00	Darwin Dinner (Cité Universitaire) 18:00 Apéro 18:30 Talk by Nicolas Perrin 19:30 Dinner and Party			

Nicolas Perrin

University of Lausanne



I have rather wide-ranging interests across the fields of Ecology and Evolution. This led me to work on a diversity of topics, from life-history theory and optimal resource allocation to the evolution of mate choice and mating systems, population genetics and phylogeography, habitat and niche modeling, and the evolution of dispersal, kin structures and social systems. Depending on topics, I have been working on a variety of animal models, including flatworms, snails, crustaceans, fishes, amphibians, birds and mammals. My present research focuses on sex-determination systems, integrating

A brief history of sexes

Sex exerts a special fascination for humans: no other species displays a more sophisticated sexuality, and gender issues occupy a central places in all cultures. In biology, sex also occupies a central and inescapable place: sexual reproduction is notably at the core of the definition of species. However, many aspects of sex remain obscure, beginning with its exact biological function. This talk will focus on questions pertaining to the biological sexes (male/female). We will first see what sexes are, how and why they evolved, and why they are only two. Second, we will discuss sex-determining mechanisms (what makes a given genome develop as male or as female). After a brief overview of the bewildering diversity of mechanisms found in nature (and of theories to account for sex determination...), I will present features of a general model aimed at integrating all potential components in a unified framework.

Anna-Liisa Laine

University of Helsinki

Our understanding of how ecological and evolutionary dynamics are played out in nature has been revolutionized by a seemingly trivial realization – all species have spatial population structures at some scale. Within a spatial framework I combine epidemiological, experimental, and molecular approaches to understand how eco-evolutionary feedback loops drive species interactions.

Much of my work is focused on understanding how diversity is maintained in host and parasite populations. Understanding this is one step closer to answering questions of how risks of virulence and pathogen occurrence evolve – important questions from both basic and applied points of view



Uncovering diversity and its drivers in a large natural pathogen metapopulation

*Uncovering how variation is distributed through space and time in pathogen populations is the key to predicting risks of infection. Although the drivers of disease occurrence are relatively well understood, far less is known about how diversity is distributed during epidemics. Here, we analyze a densely sampled longitudinal genetic dataset jointly with long-term epidemiological data in order to identify the drivers of diversity and transmission dynamics of an obligate plant pathogen, *Podospheera plantaginis*. The pathogen occurs as a metapopulation in its highly fragmented host population network in the Åland archipelago. Our results reveal a highly diverse pathogen metapopulation. Although the annual turnover rate of genetic diversity is high, there is remarkably little temporal variation in the overall level of diversity. However, we find striking variation in how diversity is distributed in space. Novel pathogen strains are most likely to emerge in populations with coinfection, resulting in spatial hotspots of outcrossing. These populations are also more likely to survive overwinter. Winter-resting spores are experimentally determined more viable when produced through outcrossing than through selfing. Jointly our results confirm that outcrossing has direct epidemiological consequences as well as a major impact on pathogen population genetic diversity, thereby promoting facultative sex in pathogens.*

Anna-Sapfo Malaspinas

University of Lausanne



Ancient and modern DNA research have both entered the genomics era. At the Evolutionary Genomics Group (EGG)/Computational Paleogenomics Group (CPG), we aim at characterizing evolutionary processes (genetic drift, natural selection, migration and mutation) while relying on genomics data from both modern and ancient samples. We develop analytical and computational methods to analyze and interpret time sampled data and we apply those methods to novel ancient DNA datasets via collaborative projects. Our work should allow to quantify and time adaptive and migration events –notably related to the human colonization of the world - while generating unique datasets.

A genomic perspective of the peopling of the first (Australia) and last (the Americas) continents being colonized by humans

While it is clear that over thousands of years anatomically modern humans have successfully colonized almost every region of the world, it remains contentious how and when they have done so. In this talk we will review some recent results related to the peopling of the first and last continents being colonized by humans once they left Africa. We will discuss open questions related to the peopling of the Americas including the number of waves necessary to explain the past and current genetic diversity. We will also discuss the key role played by Australia in understanding the out of Africa events. Finally, we will present a recent outreach project that allowed us to communicate our most recent results to children less than a year after they were published by turning our manuscript into an accessible theatre play

Raphaël Arlettaz

University of Bern

I now work primarily on societally-relevant biodiversity conservation and restoration issues, systematically applying a problem-solving approach. My current main research focus is on population biology of rare and endangered animal species (insects and vertebrates, especially birds and bats) of temperate, Mediterranean and Alpine biomes, and on community ecology (plants, invertebrates, vertebrates) of agro-ecosystems and Alpine ecosystems (grasslands, vineyards, fruit tree plantations, forests, treeline habitats and floodplain rivers).



The 6th (mass) extinction: research for action

Most conservation research focuses on describing patterns and mechanisms of species decline and ecosystem degradation, warning about an increasingly dull future for biodiversity. We need to move biological conservation research to a more meaningful activity that provides pragmatic evidence-based guidance for enhancing biodiversity preservation and restoration. I will illustrate this necessary paradigmatic and operational shift with an example from agro-ecology.

Klaus Zuberbühler

University of Neuchâtel



En 1871, le célèbre Darwin écrit que selon lui, il n'y a pas de différences fondamentales dans les capacités mentales entre l'Homme et les mammifères supérieurs. Dans les dernières décennies, cette revendication a mené à de nombreuses recherches empiriques, qui dans l'ensemble, n'ont fait qu'appuyer l'hypothèse de Darwin. Cependant, une capacité mentale a été particulièrement difficile à étudier avec le peu de progrès qui a été réalisé jusqu'à nos jours: la faculté du langage.

Un objectif principal de nos recherches est alors d'explorer et de comprendre les origines biologiques des différents mécanismes nécessaires à la langue et à la culture. Pour parvenir à nos buts, nous étudions principalement les primates non-humains dans leurs habitats naturels.

The Ethology of Primate Cognition

Current theories of animal cognition are mostly based on behavioural experiments carried out with captive primates. This is particularly true for great apes, whose cognitive abilities have been extensively investigated and compared with those of humans. Despite unprecedented progress, this line of research has limited validity because tasks are often unrelated to what subjects encounter in real-life situations, with experimental designs requiring subjects to earn food from apparatuses controlled by humans. I review recent progress with wild chimpanzees to show how field experiments can provide significant shifts in theory, including profound problems such as the evolution of culture and language.

Posters Thursday 15.2

Poster	Author	Affiliation	Title
1	JEREMY RIO	U. Geneva	Bayesian estimation of partial population continuity using spatially explicit simulations
3	MARIA WEINRICH	U. Bern	Grassland ecological quality: how do indicator plant species predict invertebrate diversity?
5	SIMON CRAMERI	ETH Zurich	Molecular species diagnosis in CITES-listed <i>Dalbergia</i> precious woods: insights and implications for forensic timber identification
7	CORINA MAURER	U. Bern	Effects of habitat fragmentation on bumblebee foraging trip duration and colony fitness
9	PETRA BENETKOVÁ	Charles University	Community development of soil nematodes during heathland restoration in the Netherlands
11	CLAUDIA BLUMENSTEIN	U. Bern	The effect of lamp proximity to aquatic habitats on the attraction of adult aquatic insects
13	SIMON TRESCH	U. Neuchatel	What drives the decomposition of organic material in urban gardens?
15	ANAÍS BINGGELI	U. Bern	Foraging micro-habitat selection of the White-Winged Snowfinch <i>Montifringilla nivalis</i> in the Swiss Alps
17	MATHILDA HAYOZ	U. Neuchatel	Endospores in paleoecology: Investigation of their origin in high mountain lakes
19	BENEDIKT SCHMIDT	Info Fauna Karch, U. Zurich	Amphibian decline in protected areas
21	CLAUDIO AUGUGLIARO	U. Lausanne	Snow leopard site use in the Mongolian Altai-Sayan Ecoregion: the effects of preys and sympatric large carnivores
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Oral presentation abstracts

Oral Presentations Abstract Book

The reticulate evolution of Lake Victoria cichlids

Joana Meier, University of Bern
Ole Seehausen, EAWAG

The African Lake Victoria region harbors adaptive radiations in multiple lakes encompassing 700 species. This “Lake Victoria Region Superflock” (LVRS) evolved in only 150,000 years from admixed ancestry between Congolese and Nilotic cichlids. The largest LVRS radiation occurs in Lake Victoria, which refilled after desiccation 15,000 years ago. Today, Lake Victoria harbors 500 endemic species occupying all trophic levels from algae scrapers to piscivores. By resequencing 450 genomes of cichlids in Lake Victoria and neighboring lakes, we investigate the evolution of this astonishing radiation. We find that Lake Victoria cichlid species cluster by ecological similarity indicating that ecological guilds emerged early in the radiation. Together, they form a genetic cluster, distinct from all other lake radiations. The large ecological diversity thus evolved within the lake and not from independent colonizations of ecologically divergent species. However, we find evidence for >2 colonizing lineages which admixed prior to the onset of the radiation. We also detect hybrid origin of distinct species and an entire ecological guild. Hybridization thus played an important role at multiple levels in the history of these cichlids: 1) 150kya, Congo-Nilotic admixture gave rise to the entire LVRS, 2) 15kya, admixture between several LVRS lineages fueled the modern Lake Victoria radiation, and 3) hybridization between modern Lake Victoria species gave rise to new species and ecological guilds.

Oral presentation abstracts

Adaptation and Genomics

Combining transcriptomic and fitness data to study plastic and evolved responses to environmental changes

Eva Koch, University of Zürich

Frédéric Guillaume, University of Zürich

Whole transcriptome sequencing has become a powerful tool giving us detailed insights into physiological processes underlying plastic as well as evolutionary responses. However, it is challenging to understand how certain components are ultimately linked to fitness and adaptation. We therefore measured gene expression using RNA-seq and fitness to study the plastic and evolved responses in *Tribolium castaneum* to understand the role of gene expression for adaptation. We used two different stressors (drought and heat) and the combination of both. Heat resulted in a stronger reduction of fitness and a larger number of differently expressed genes compared to drought. Furthermore, overlap between both responses was small and different pathways were affected. The joint stress response included most of the genes found in single stress treatments. Combining fitness and expression data, we further identified condition specific modules of co-expressed genes that were related to fitness and estimated selection gradients on single gene expression levels. Using experimental evolution we tested for adaptation to all conditions after 20 generations and found that selection lines were able to increase their offspring number. When we compared responses in gene expression we found that plastic responses were opposite to the evolved responses. Furthermore, selection intensity on gene expression levels in the first generation and the evolved changes in expression were positively correlated.

Oral presentation abstracts

Adaptation and Genomics

Recent adaptive evolution through segmental duplications in a semi-clonal fungal pathogen

Luzia Stalder, University of Neuchâtel

Norfarhan Mohd-Assaad, ETH Zürich

Daniel Croll, University of Neuchâtel

Microbial pathogens can rapidly adapt to changing environments such as the application of pesticides or novel host resistance. Sexual reproduction greatly facilitates the fixation of beneficial mutations through meiotic recombination. Yet, many microbial pathogens undergo predominantly clonal reproduction and adaptive genetic variation mostly originates from dynamic karyotypes. How duplications and deletions influence adaptive evolution in natural populations is poorly understood. Here, we analyze how populations of *Rhynchosporium commune*, a pathogen with a mixed reproductive strategy and the causal agent of barley scald, adapted to environmental challenges. We screened the genomes of 114 worldwide isolates for robust evidence of gene copy number variation (CNV). We identified a total of 7879 gene duplications and 116 gene deletions. The majority of gene duplications likely resulted from chromosomal duplications. Using a comparative genomics framework, we found that CNVs generated by recent gene losses were enriched in genes encoding proteins that likely manipulate the host physiology (i.e. effectors). In contrast, CNVs generated by recent gene gains were enriched in genes encoding cell wall degrading enzymes. We performed a phylogeny-informed genome-wide association study and identified CNVs that were significantly associated with adaptive phenotypic trait variation. We found that a very recent duplication of *CYP51A*, a gene encoding the target protein of azole fungicides, significantly contributed to the emergence of azole resistance. The rapid amplification of genes encoding proteins targeted by fungicides was previously only observed during intra-host evolution of human pathogens. Overall, our study demonstrates how natural populations of a semi-clonal plant pathogen adapt to environmental challenges through extensive segmental duplications.

Oral presentation abstracts

Adaptation and Genomics

The architecture of adaptation: a mass of mutations or a master mutation?

Sophie Archambeault, University of Bern, University of Washington

Luis Bärtschi, University of Bern

Catherine L. Peichel, University of Bern

Genomic mapping of the loci of phenotypic evolution in multiple organisms has revealed genomic “hotspots”, or regions of the genome that control more traits than expected. This clustering of traits has important implications for the speed of adaptation, and could be due to pleiotropic effects of a single mutation or tight genetic linkage of multiple causative mutations. The threespine stickleback (*Gasterosteus aculeatus*) is a powerful model for the study of adaptive evolution because the marine ecotype has repeatedly adapted to freshwater environments across the northern hemisphere in the last 12,000 years. This adaptive process has resulted in the repeated fixation of a 16 kilobase genomic hotspot on chromosome IV that affects multiple traits, including defensive armour, sensory hair cells, and schooling behaviour. We have performed association mapping in a fully interbreeding, polymorphic population of freshwater stickleback in order to disentangle the relationships between genotype and phenotype in this genomic hotspot. Our findings suggest that the coordinated phenotypic changes are due to both pleiotropic effects of a single mutation and tight linkage of multiple causative mutations.

Oral presentation abstracts

Adaptation and Genomics

Genetics of parasite resistance in a co-evolving population

Camille Ameline, University of Basel

Yann Bourgeois, New York University in Abu Dhabi

Dieter Ebert, University of Basel

Host-parasite coevolution is a major driver of diversity in nature. It is driven by genotype-specific host-parasite interactions. To better understand these interactions, the genetics of host resistance and parasite infectivity must be investigated. We were interested in resolving the genetics of parasite resistance in a focal, long-term monitored population of *Daphnia magna* (Crustacea: Cladocera) undergoing seasonal epidemics of *Pasteuria ramosa* (Firmicutes: Bacillales) in a large Swiss pond. We investigated parasite resistance both phenotypically and genotypically at a particular locus via an association study and genetic crosses. In addition, we studied the evolutionary dynamics of resistance in the focal population again both phenotypically and genotypically. We found that most variation in resistance phenotypes (resistotypes) is shaped by the presence of two physically unlinked, strongly epistatic loci. We observed pronounced frequency changes of resistotypes linked to strong parasite-driven selection in these loci. Altogether, this study provides insights into the evolutionary genetics of resistance in a population undergoing strong host-parasite coevolution.

Oral presentation abstracts

Adaptation and Genomics

Genomics of host-virus coevolution

Cas Retel, Eawag, Fish Ecology and Evolution; University of Bern, Aquatic Ecology

Vienna Kowallik, Max Planck Institute for Evolutionary Biology

Lutz Becks, Kiel Evolution Center, Community Dynamics; Max Planck Institute for Evolutionary Biology

Philine Feulner, Eawag, Fish Ecology and Evolution; University of Bern, Aquatic Ecology

Dramatic population size fluctuations are often observed in coevolving systems, but it is to a large extent unknown how this affects genomic variation and evolution at the molecular level. Understanding how demographic processes, selection and their interplay shape genomic variation is particularly interesting when adaptation of one species affects population size of the other and vice versa (eco-evolutionary dynamics).

We use an experimental setup where host (*Chlorella*) and virus (*Chlorovirus*) populations reciprocally evolve resistance and virulence mechanisms over 90 days. Previous research has shown demographic and ecological dynamics closely matching across multiple replications of coevolution. Starting with clonal populations, they initially reflect an "arms race" and later change into a state where both species co-occur at stable densities, but phenotype abundances within populations fluctuate.

We now reveal the temporal genomic signature of this coevolutionary process. Whole-genome data for both species for 10 time points allowed us to identify and track the alleles with frequency changes driven by selection. Using data from three replicates, we find evidence for non-constant selection, parallel genetic changes and the importance of genomic background. We further reveal consistent differences in the dynamics of molecular changes between the two species. The observed demographic and phenotypic reproducibility is produced by complex underlying genomic dynamics.

Oral presentation abstracts

Adaptation and Genomics

Parallel adaptation to climate in quaternary lineages of North American *Arabidopsis lyrata*

Nora Hohmann, University of Basel

Kay Lucek, University of Basel

Yvonne Willi, University of Basel

Whether adaptation to similar habitats is caused by selection from standing genetic variation or by parallel evolution is one of the fundamental questions in evolutionary biology. Today's distribution of North American *Arabidopsis lyrata* subsp. *lyrata* is shaped by periglacial survival in two refuge areas and post-glacial range expansion, resulting in two distinct genetic clusters that have been separated for at least one glaciation cycle and thus provide an ideal system to study parallel adaptation to climate. We investigated adaptation related to various climatic variables in these two genetic clusters. Generally, we observed little overlap between loci affected by adaptation to climate on the level of single nucleotide polymorphisms (SNPs) or genes. However, overlap was extensive on the level of gene ontology (GO) terms, suggesting independent, parallel adaptation. Overall, our results exemplify that different evolutionary solutions to the same problem can underlie apparent phenotypic parallelism.

Oral presentation abstracts

Adaptation and Genomics

Genomics of ancient Brazilian populations

Cruz Dávalos Diana Ivette, University of Bern and University of Lausanne
Anna-Sapfo Malaspinas, University of Lausanne

When the Portuguese settlers arrived in Brazil, they named “Botocudos” the Central-Eastern inhabitants who wore wooden lip and ear plates. The Botocudos actually comprised several cultural groups speaking distinct languages. Most of the Botocudo groups became extinct by the end of the 19th century, when the Portuguese Crown declared war to all indigenous tribes that refused to accept the regime. The National Museum of Rio de Janeiro owns a collection of 35 Botocudo skulls. While analyzing the mitochondrial DNA of 14 of these samples, Gonçalves et al. identified two individuals with Polynesian haplogroups. The ancestry of those individuals was further explored at the nuclear level by Malaspinas et al., who determined that both samples had a Polynesian ancestry without signs of admixture from Native American or African populations. Several scenarios were put forward to explain those results including that these individuals arrived in the Americas as part of the Polynesian expansion, or as crew or passenger members in European ships. Here, we report preliminary genomic data from 21 individuals from the Botocudo collection. We performed population genetic analyses to characterize and identify the population structure of those samples. Finally, we specifically look into whether any of our samples had a genetic affinity to non-Native American populations.

Oral presentation abstracts

Behaviour

Divergent brain gene expression profiles between alternative behavioural helper types in a cooperative breeder

Claudia Kasper, University of Bern

Francois-Olivier Hebert, Université Laval, Québec

Nadia Aubin-Horth, Université Laval, Québec

Barbara Taborsky, University of Bern

Juveniles of the cooperatively-breeding cichlid fish *Neolamprologus pulcher* either consistently provide help in form of alloparental egg care ('cleaners') or consistently abstain from helping ('non-cleaners'). These phenotypes are not based on heritable genetic differences. Instead they arise during ontogeny, which should lead to differences in brain structure or physiology, a prediction that is currently untested. We compared brain gene expression profiles of cleaners and non-cleaners in two experimental conditions, a helping opportunity and a control. We compared gene expression between cleaners and non-cleaners in the control and gene expression induced by the opportunity, and plasticity of gene expression between cleaners and non-cleaners. Cleaners and non-cleaners during the control differed in the expression of a single gene, *irx2*, which regulates neural differentiation. Cleaners and non-cleaners expressed partly overlapping and partly unique sets of genes during the opportunity compared to their respective controls, including genes implicated in neuroplasticity, hormonal signalling and cell proliferation. We found evidence that behavioural specialization is associated with subtle, but long-lasting differences in resting brain gene expression profiles, which provides insight into the development of different helper phenotypes during ontogeny. Our results indicate that both behavioural types responded to the helping opportunity, but in a distinct way.

Oral presentation abstracts

Behaviour

When in doubt, observe your parents!

Mukta Watve, University of Bern

Barbara Taborsky, University of Bern

Social learning of predation pressure during early ontogeny can be beneficial in developing appropriate anti-predator behaviors. Parents can either intentionally signal risk levels to offspring or the offspring can indirectly infer ambient risk levels from parental defense behavior. Presence of parents during early development is known to shape more appropriate social behavior in the cooperatively breeding cichlid *Neolamprologus pulcher*. It is however unknown whether parents also influence behavior towards heterospecifics, particularly predators. To test this, we split sibling groups in half and raised them with or without parents. Both rearing groups repeatedly received visual and olfactory cues from four types of fish (predators, egg-predators, herbivores and conspecifics) for 4 weeks. After a 'neutral phase' of 4 months in identical conditions, individuals from both rearing conditions were tested for their response towards the same four stimulus species. Unlike those reared without parents, the fish reared with parents spent significantly more time in safety and were more vigilant towards the predator, whereas responses to the other species did not differ. Our results show that the presence of parents boosts an appropriate response towards a high-risk predator. As there is no direct parent-offspring interaction in *N. pulcher*, the presence of parents most likely only heightens the sense of impending risk in the offspring, which in turn develop better predator evasion.

Oral presentation abstracts

Behaviour

Wild vervet monkey screams inform potential helpers on caller's social role and conflict severity

Stéphanie Mercier, University of Neuchâtel

Eloïse Déaux, University of Neuchâtel

Erica van de Waal, University of Lausanne & University of Zurich

Axelle Bono, University of Lausanne

Klaus Zuberbühler, University of Neuchâtel & University of St Andrews

Screams are specific high-pitched long distance calls produced by many species. Despite the wide range of context production, they share a similar acoustic structure that primarily serves to influence receivers. However, screams are also highly variable and this variation may relate to the identity of signallers and the nature of the ongoing event. Although vervet monkey screams are flexible in context production and show individual distinctiveness meaningful to receivers, the influence of social and contextual factors on their acoustic structure has not been explored. We examined 12 parameters of 306 agonistic screams produced by 28 wild vervet monkeys to investigate whether acoustic variation was predicted by the social role of signallers and/or conflict severity. Results from linear models showed that those two factors influenced six out of the 12 acoustic parameters analysed. Post-hoc analyses demonstrated that individual characteristics, such as the age-sex class of signallers, also explained part of this variation. While keeping a general unpleasant structure helps signallers to reduce the aggression level by repelling their opponents, the variation found in some other acoustic features, in contrast, may help to attract potential helpers that can decide to intervene only when necessary, that is, when a kin or important social partner need support.

Oral presentation abstracts

Behaviour

Awareness of danger in cuttlefish embryo

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Nawel Mezrai, EthoS - Université de Caen Normandie

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Predation exerts one of the greatest selective pressures on prey organisms. Many studies showed the existence of innate anti-predator responses mostly in early stages of juveniles vertebrate and from olfactory cues. Learning is also possible, but risky. There is now growing evidence that embryonic learning exists in animals but few studies have tested for learning in embryos. Here, we show that *Sepia pharaonis* cuttlefish embryos react to both the odor and the sight of a predator fish but not to those of a non-predator fish. Interestingly, embryos can also learn to associate a non-threatening stimulus with a threat, cuttlefish ink or a carnivorous fish odor. After several paired exposures, they respond to the harmless fish as if it were dangerous. Our results demonstrate both visual and chemical innate predator recognition in a cephalopod. This is the first demonstration of sensory awareness in an invertebrate embryo. Last, our result is the first report of associative learning in an invertebrate embryo. This shows that cuttlefish embryos have both, genetic predator avoidance skills and possess enough cognitive plasticity to learn and retain new threats before hatching. The combination of these mechanisms is an impressive example of the early adaptability of cephalopods. This amount of behavioural plasticity gives the newly-hatched *Sepia* a huge selective advantage when dealing with known or new threats. These results broaden a new field of research about cognition in embryos.

Oral presentation abstracts

Biotic Interactions

Local adaptation of plant-herbivore interactions along a soil fertility gradient

Anne Kempel, Swedish University of Agricultural Sciences Umea

David Wardle, Swedish University of Agricultural Sciences Umea

Environmental variation and biotic factors can exert strong selective pressures on plants. This can lead to local adaptation by natural selection. However, the drivers of local adaptation often remain unidentified, and very little is known about the potential contribution of biotic factors, such as herbivores, to local adaptation. In a large reciprocal transplant experiment with seedlings of *Betula pubescens* originating from an island chronosequence in northern Sweden, we tested whether plants along a soil fertility gradient are locally adapted, and whether the drivers of local adaptation are abiotic or biotic. The 30 islands of the chronosequence are all of the same geologic age, and only differ in wildfire frequency through lightning strike, which generates a soil fertility gradient. Our preliminary results show that indeed plants perform best, and were also less damaged by herbivores, when growing on their home islands. Additionally, plants transplanted to nutrient poor islands had more herbivore damage than plants transplanted to nutrient richer islands, indicating higher herbivore pressure on nutrient poorer islands. Concordantly, plants originating from nutrient poor islands showed less herbivore damage when transplanted to other islands, assuming higher resistance in these plants. Our preliminary results indicate that plants might be locally adapted to different amounts of herbivore pressure, and offers general insights into plant defense strategies.

Oral presentation abstracts

Chemistry and Interaction

Floral volatiles and corresponding transcript expression of brood-site mimic, *Arum maculatum*, are geographically structured and vary according to the dominant pollinator species

Adrienne Godschalx, Université de Neuchâtel

Mark Szenteczki, Université de Neuchâtel

Sergio Rasmann, Université de Neuchâtel

Nadir Alvarez, Natural History Museum of Geneva

Coercing insects to carry genetic material from one plant to another has resulted in many specialized adaptations, often taking advantage of the pollinator's life history. Brood-site mimicry in the *Arum* genus traps dung-seeking pollinators by producing heat and volatilizing feces-like fragrances. Volatile suites vary by species, attracting unique pollinator species, but variation in volatiles within a species targeting different pollinator species in a putatively adaptive manner has not been shown for floral scent. Two fly species from the genus *Psychoda* are mainly trapped by *Arum maculatum* across Europe, with *P. phalaenoides* and *P. grisescens* dominating inflorescences in northern and southern regions, respectively. To analyse differences in plant volatile production across Europe, we collected dynamic headspace volatiles using stir bar sorptive extraction, followed immediately with spadix tissue sampling for transcriptomic analysis from plants from populations throughout France, Italy, and the Balkans. We found significant population-level differences in the volatile suites as well as in the overall transcriptome of the inflorescences. In addition, we found that fly specialization coincided with variation in the volatile blend, suggesting pollinator-driven local adaptation in odors mediating deceptive pollination.

Oral presentation abstracts

Chemistry and Interaction

Wasps with a chemical invisibility cloak

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Christoph Vorburger, Eawag Dübendorf

Mark Mescher, ETH Zürich

Consuelo De Moraes, ETH Zürich

Aphids are among the world's most important and economically damaging agricultural pests. A frequently used biological control strategy involves parasitoid wasps. These wasps efficiently reduce aphid numbers, provided that there are no ants present. Ants live in a mutualistic relationship with aphids and get sugary honeydew in exchange for effective protection against aphid enemies. Most parasitoid wasps get attacked by ants but wasps from the genus *Lysiphlebus* are ignored. The ants cannot distinguish between aphids and wasps because the latter use a chemical invisibility cloak. The compounds involved in this chemical mimicry are cuticular hydrocarbons (CHC), which not only waterproof the insect cuticle but also play a major role in insect communication.

A field survey sheds light on the variability and similarity between *Lysiphlebus* wasp CHCs and their host aphid profiles. We included *Lysiphlebus* from eight different aphid species. After extracting the CHCs from wasps and their hosts the samples were analyzed by gas chromatography-mass spectrometry to get qualitative and quantitative CHC profiles. The most important compounds separating the profiles of the different aphid species were methyl alkanes, which were also the compounds best separating the profiles of wasps from different hosts. This is a first indication that methyl alkanes are the key compounds in this chemical mimicry system. Behavioral experiments with ants will be used to confirm this hypothesis.

Oral presentation abstracts

Chemistry and Interaction

Another one bites the leaf: Heterophylly of Mascarene plants as an adaptation to giant tortoise herbivory

Andrin Dürst, University of Zurich

Aurèle André, Francois Leguat Giant Tortoise and Cave Reserve

Christine J. Griffiths, Ebony Forest Ltd.

Arnaud Meunier, University of Zurich

Dennis M. Hansen, Francois Leguat Giant Tortoise and Cave Reserve, University of Zurich

Heterophylly is a widespread phenomenon found in many different plant families and outstandingly prominent among the Mascarene islands, especially on Mauritius and Rodrigues. Here, many endemic plants have two leaf types (juvenile and adult) that are strikingly different (size, shape and colour). At some height above ground, typically between 0.8–1.5 m the leaves abruptly change its appearance. This feature has been proposed to be an adaptation to herbivory by recently extinct giant tortoises (*Cylindraspis* spp., the largest of which could browse up to ~1.3m). Studies in Mauritius revealed that introduced non-native Aldabra giant tortoises (*Aldabrachelys gigantea*) could distinguish between the two leaf morphs, strongly preferring the adult leaves, but an analysis of secondary chemical compounds in dried leaves didn't find a clear pattern. Expanding our understanding of the generality of tortoises' response to Mascarene heterophylly, we studied the feeding response of tortoises to heterophyllous leaves from nine endemic plant species from Rodrigues. We included an ontogenetic aspect by using three different age classes of tortoises. Our choice experiments highlighted that Aldabra giant tortoises at any life stage can distinguish between the two leaf types and prefer adult-type leaves over juveniles. Our findings lend further support to the hypothesis that heterophylly has evolved multiple times independently as an anti-tortoise defence strategy of Mascarene plants.

Oral presentation abstracts

Chemistry and Interaction

A small microbial community for the degradation of a pollutant

Philippe Piccardi, University of Lausanne

Sara Mitri, University of Lausanne

Manufacturing activity is unfortunately often associated with the production of toxic wastes, which are endangering both our health and the environment. Bioremediation, where microbes degrade polluted products, represents a great opportunity to solve this ecological problem in a low-cost and eco-friendly way. In our research, we are studying how microorganisms digest pollutants from metal-working fluids (MWF), a coolant and lubricant employed in the manufacturing industry. From previous research [1, 2], we obtained a synthetic bacterial community consisting of four strains capable of degrading MWF compounds. Here, I show the methods that we established to accurately and repeatedly determine the bacterial abundance in the MWF ecosystem and, in parallel, to evaluate the reduction of the pollution load. Our preliminary results show that the four-species community is more efficient at detoxifying MWF compared to when each species is cultivated alone. Interestingly, it seems that some species need the presence of the others to survive, grow and contribute to the process of detoxification. Together, these observations suggest that bacterial interspecies interactions are important in determining the dynamics within this simple ecosystem. The next and exciting goal of this project is to elucidate why this system works and how we can deliberately interfere with it to make it more powerful and efficient.

Oral presentation abstracts

Conservation

Effects of habitat quality and fragmentation on Woodlarks (*Lullula arborea*) and their invertebrate prey in intensively managed vineyards

Laura Bosco , University of Bern

Ho Yi Wan, Northern Arizona University

Samuel A Cushman, Rocky Mountain Research Station

Raphaël Arlettaz, University of Bern

Alain Jacot, University of Bern

Vineyards in Switzerland are among the most intensively managed crop systems. The vast majority of all parcels are treated with herbicides and do not have ground vegetation. Differences in management lead to a fragmented system of few vegetated parcels embedded within bare parcels. The Woodlark (*Lullula arborea*) is an endangered insectivorous bird species that has its Swiss stronghold in this intensively managed agroecosystem. In a first study we assessed Woodlarks' habitat preferences and linked their occurrences to their invertebrate prey. Woodlarks showed a clear preference for vegetated vineyards with higher abundance and richness of invertebrate prey, increased plant richness and wider inter-row distances. Given the importance of invertebrates for Woodlarks, we then investigated the effects of fragmentation (number of vegetated patches) and habitat amount (area of vegetated patches) on invertebrate abundance. Our findings demonstrate that fragmentation impedes the movement of invertebrates, as in areas with less habitat, fragmentation negatively affects their abundance. Further, a multi-scale habitat suitability analysis revealed that, inter alia, the small scaled extensiveness of vegetated patches seems to be a strong driver of invertebrate abundance. Our results suggest that the installation of a network of well-connected vegetated patches with increased plant richness may promote invertebrate abundance and richness and thus improve the habitat matrix for the Woodlark.

Oral presentation abstracts

Conservation

The invasive plant *Impatiens glandulifera* affects soil fungal diversity and the bacterial community in forests

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Hans-Peter Rusterholz, Section of Conservation Biology, Department of Environmental Sciences, University of Basel

Bruno Baur, Section of Conservation Biology, Department of Environmental Sciences, University of Basel

Invasive plants may severely impact native biodiversity and ecosystem functioning. We examined potential effects of the invasive annual plant *Impatiens glandulifera* Royle on soil fungal and bacterial communities in forests in Northwestern Switzerland. Using a space-for-time approach, we established 72 plots in forest areas invaded by *I. glandulifera* and in forest areas, which were not yet invaded, equally distributed over three coniferous and three deciduous forests. In each plot, we determined plant species richness and abundance in the above-ground vegetation as well as the diversity and composition of the soil fungal community using T-RFLP analysis. Biolog Ecoplates were used to assess the activity of soil bacteria. The invasion of *I. glandulifera* caused significant shifts in plant species composition. Invaded plots were characterized by a higher diversity and an altered composition of the soil fungal community and by a lower soil bacterial activity in late spring. Carbon substrate utilization patterns of soil bacteria were also changed in invaded plots. Our experiment shows that *I. glandulifera* can modify soil fungal and bacterial communities, probably as an indirect effect of altered soil properties induced by the invasive plant, combined with the release of allelopathic compounds into the soil.

Oral presentation abstracts

Conservation

Consequences of long-term organic farming on yield and environmental performance

Chantal Herzog, Agroscope

Adrian Honegger, Agroscope

Raphaël Wittwer, Agroscope

Django Hegglin, Agroscope

Hans-Rudolf Oberholzer, Agroscope

Anne de Ferron, Agroscope

Philippe Jeanneret, Agroscope

Marcel van der Heijden, Agroscope

In agro-ecosystems, research is currently seeking for management systems that guarantee food security and simultaneously minimize environmental impacts. In Switzerland, organic farming is gaining importance but despite its beneficial effects on soil health, environmental performance and biodiversity, it is still unclear whether the duration of organic farming influences yield and environmental services. To tackle this knowledge gap, we investigated 34 fields within a farmer network, divided in four farm categories – conventional management, recently converted, and “new” and “old” organic farms, in two subsequent years with the aim to test whether the duration of organic management affects plant yield, weed populations, soil fertility and biodiversity. Our results show that 1) crop yield is lower in organic compared to conventional fields. Importantly, the duration of organic management did not affect plant yield, which remained constant irrespective of management duration; 2) similar effects were observed for weed pressure but with strong variations among fields; 3) soil fertility was maintained over time; 4) spider abundance correlated with weed coverage but did not differ between organic and conventional fields; and 5) root colonization by arbuscular mycorrhizal fungi was higher in organic compared to conventional fields in the second study year. Overall, this study shows that the duration of organic farming practices has no negative impact on yield or soil fertility.

Oral presentation abstracts

Conservation

Terrestrial habitat fragmentation determines abundance of aquatic salamander larvae

Oliver Dosch, University of Zurich

Arpat Ozgul, University of Zurich

Benedikt R. Schmidt, University of Zurich, Info fauna karch

Habitat complementation is defined as the use of different habitat types by species with complex life cycles. For instance, aquatic breeding amphibians rely on habitat complementation; both aquatic and terrestrial habitats must be available. While the limits of the aquatic habitat are easily defined, the spatial extent of the terrestrial habitat is less well known. To achieve a better understanding of the spatial scale of the terrestrial habitat and consequently habitat complementation, it is necessary to quantify the effect of habitat characteristics at different spatial scales. In this study we analysed the habitat variables explaining spatial variation in abundance at multiple spatial scales. We estimated larval abundances of *S. salamandra* in 50 streams in a semi-natural landscape. We found strong spatial variation in abundance, which was best explained by a combination of variables at different scales. My top-ranking model showed a positive effect of the length of pools per stream section, a negative effect of a forest fragmentation index at the 200m scale, and a negative effect of narrow tarred roads at the 1km scale on salamander larvae abundance. Thus, anthropogenic habitat modification drives local variation of the abundance of larvae in streams. My results show the importance of investigating multiple scales and the need for incorporating the concept of habitat complementation in ecological studies on species with complex life cycles.

Oral presentation abstracts

Conservation

Conservation of endangered plants: a roadmap for the selection of translocation sites

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Yannick Storrer, SFFN, Neuchâtel

Sergio Rasmann, Université de Neuchâtel

The conservation translocations of endangered plant species have become increasingly used techniques for withstanding the increase of species loss worldwide. However, a comprehensive approach that merges natural history with modern modelling techniques to identify suitable restoration sites does not exist today. I propose here a hierarchical and holistic roadmap to identify appropriate reintroduction and introduction sites. Step 1 includes modelling of present and future bioclimatic and topographical niches of target species. Step 2 consists in analysing ecological parameters (i.e. vegetation or soil) in reference populations. In addition, life history traits of the target species are measured in order to establish a connexion between those biological traits and favourable environmental factors. Data are then statistically analysed to extract the most important parameters for the species' ecology. Step 3 is dedicated to the improvement of prediction maps obtained in step 1 using field data gathered in step 2. In order to illustrate this methodology, this study focuses on the Lady's slipper Orchid (*Cypripedium calceolus* L., Orchidaceae) growing in Switzerland, for which conservation plans have existed for years, but generally unfruitful. This work can be considered as the basis of a broader roadmap that will include more ecological factors, such as biological, historical and demographical ones, in order to lead to more accurate identifications of suitable translocation sites.

Oral presentation abstracts

Cooperation

Variation in human cooperation: Key proximate mechanisms

Jennifer McClung, UniNE

Redouan Bshary, UniNE

While we know that human cooperation supersedes other species, its variation has yet to be fully explained, possibly because research based on experimental game-theoretical paradigms neglects fundamental features of human life, namely social interaction and language. Using a new optimal foraging game loosely modeled on the prisoner's dilemma, the Egg Hunt, we categorized players as either in-group or out-group to each other and allowed them to make interactive, potentially cooperative decisions. We assessed players' spontaneous helping decisions and the language they used during the hunt, as well as their endogenous levels of the neurohormone oxytocin (OT) before and after the hunt. Both shared group membership and the possibility to talk led to increased cooperation and overall success in the hunt. Analysis of players' conversations showed that in-group members engaged more in shared intentionality, the human ability to mentally represent and then adopt another's goal, and that this mechanism directly drove the increase in helping between in-group players. OT also promoted this cooperation: higher baseline OT predicted more helping during the hunt between in-group members whereas out-group players helping was not affected by OT. In sum, we have identified a psychological and a hormonal mechanism, shared intentionality and oxytocin, that drive successful cooperation in particular social contexts, suggesting probable sources of the variation in cooperation humans display.

Oral presentation abstracts

Cooperation

Too hungry to cooperate – influence of drought on sentinel behaviour and its vocal coordination in meerkats

Ramona Rauber, University of Zurich

Tim Clutton-Brock, University of Cambridge

Marta Manser, University of Zurich

Harsh, arid habitats are key factors in the evolution of cooperative breeding and are commonly associated with high levels of environmental uncertainty including extreme droughts. Droughts reduce resource availability, leading to reductions in body condition and ultimately increases mortality. However, the effect of extreme environmental conditions on cooperative behaviours is unknown. We investigated the effect of drought on the frequency of cooperative vigilance behaviour (sentinel behaviour) and its vocal coordination in meerkats (*Suricata suricatta*). Drought conditions decreased an individual's probability and duration to go on guard, with the strongest decline in young individuals, males and members of small groups. This suggests that the costs of cooperative behaviours increase during demanding environmental conditions and, as a consequence, animals shift to behaviours that enhance direct individual survival. During the drought meerkats responded stronger to playbacks of sentinel 'all-clear' calls and contact calls seemed to take over the function of sentinel 'all-clear' calls, both resulting in less vigilance and more foraging behaviour. This indicates flexible behavioural responses to specific vocal signals based on temporary ecological conditions. We conclude that extreme environmental conditions shift the investment from cooperative behaviour to behaviours with immediate individual gain and therefore strongly affect the vocal coordination in cooperative breeders.

Oral presentation abstracts

Cooperation

Trading of Different Commodities in a Cooperatively Breeding Fish

Jan Naef, University of Bern

Michael Taborsky, University of Bern

Reciprocal altruism can explain cooperation between unrelated individuals, but the division of labour and the exchange of different commodities has mainly been looked at for related individuals. In cooperatively breeding cichlids, unrelated subordinate individuals pay to stay in the territory of dominants, and both sides of this reciprocal exchange use different commodities. We studied interactions between unrelated individuals of *Neolamprologus pulcher*, a cooperatively breeding fish in which helpers participate in brood care, territory defence and maintenance. In groups consisting of a breeding pair and one unrelated helper, we manipulated two helping behaviours (territory maintenance and defence) independently from one another and observed the effect on the reciprocal exchange between dominants and subordinate. We find that helpers who are prevented from providing one commodity will compensate this debt later on by using the same commodity, but they do not compensate simultaneously by using a different commodity. Punishment by breeders is not influenced by the commodity with which the helper pays. This implies that breeders can solve the currency conversion problem by accepting different commodities, but helpers cannot flexibly switch between these.

Oral presentation abstracts

Cooperation

How ambrosia beetles predict the weather and what this can teach us about the evolution of cooperation

Jon Andreja Nuotclà, University of Bern

Michael Taborsky, University of Bern

Delayed dispersal of sexually mature offspring is a prerequisite for helping behaviour in cooperative breeders. Nevertheless, at some stage helpers disperse to reproduce independently elsewhere. Theory predicts that dispersal decisions should be based on information about the relative fitness effects to be expected when dispersing or staying at home. Thus, knowing the criteria by which helpers decide when to cease cooperation for leaving their natal group are of crucial importance for understanding the evolutionary mechanisms of sociality in cooperative breeders.

Cooperatively breeding ambrosia beetles dwell deeply inside the heartwood of trees, where possibilities to obtain information about the environmental dispersal conditions are very limited. Nevertheless, our field and laboratory experiments show that the beetles effectively predict upcoming weather conditions and time their dispersal accordingly. We found that they delay dispersal in response to barometric pressure changes, apparently in order to avoid wind and rain, which would compromise their search for suitable host trees. We discuss how such plastic responses to perceived outside information may have facilitated the evolution of cooperation in ambrosia beetles.

Oral presentation abstracts

Ecology and Life History Traits

Density-dependent dispersal strategies in a cooperative breeder

Nino Maag, University of Zurich

Gabriele Cozzi, University of Zurich

Tim Clutton-Brock, University of Cambridge

Arpat Ozgul, University of Zurich

Dispersal is a key ecological process that influences the dynamics of spatially and socially structured populations and consists of three stages: emigration, transience, and settlement. Each stage is influenced by different individual, social and environmental factors. Despite our appreciation of the complexity of the process, we lack a firm empirical understanding of the underlying mechanisms. We studied the influence of population density, mate availability, and dispersing coalition size on each of the three stages of dispersal in a cooperative breeder, the Kalahari meerkat, by fitting GPS radio-collars to 65 dispersing female coalitions. High population density reduced daily emigration and settlement probabilities, and increased transience time. Daily emigration and settlement probabilities increased with increasing female coalition size and in presence of unrelated males. Coalition size and presence of unrelated males decreased dispersal distance. Our work demonstrates negative density-dependent dispersal in a cooperative breeder and supports existing theory proposing population density to be an important factor driving the evolution of delayed dispersal and philopatry in cooperative breeders. We give a comprehensive description of each stage of dispersal and provide a complete mechanistic study of dispersal in a wild population.

Oral presentation abstracts

Ecology and Life History Traits

Maternal effects and early developmental changes in gene expression in polymorphic Arctic charr (*Salvelinus alpinus*)

Samantha V. Beck, Hólar University College and University of Iceland

Katja Räsanen, Eawag

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Skúli Skúlason, Hólar University College

Bjarni K. Kristjánsson, Hólar University College

Camille A. Leblanc, Hólar University College

Changes in gene expression underlying developmental processes are a fundamental source of phenotypic variation and facilitators of adaptive diversification. Maternal effects, particularly those related to egg size, are important during early life-stages but their contribution to gene expression and individual development is poorly understood. In polymorphic Arctic charr (*Salvelinus alpinus*), differential distribution of maternal resources (i.e. variable egg sizes within and among clutches) can influence offspring morphology and feeding behaviour. This suggests that variation in egg size, jointly with developmental plasticity and gene expression, may facilitate evolution of resource polymorphism. We studied a polymorphic Arctic charr population that has large variation in egg size to test this hypothesis. We predicted that smaller embryos (i.e. from small eggs) have higher expression of genes related to growth and skeletal development – to compensate for lower maternal resources - compared to larger embryos (i.e. from larger eggs). Contrary to our predictions, we found that expression of two genes (MMP9, a skeletal gene, and SGK1, a growth gene) was higher in larger eggs (at post-fertilisation and hatching stage, respectively), whereas expression levels of 12 further genes were not associated with egg size. We discuss the implications of these findings for adaptive diversification.

Oral presentation abstracts

Ecology and Life History Traits

Tradeoffs between predation and growth determine differential migration

Philip Dermond, EAWAG, University of Bern

Carlos Melian, EAWAG

Jakob Brodersen, EAWAG

Every year across the globe, billions of individuals across the animal kingdom endeavor on spectacular migrations. These migratory animals take advantage of different profitability of alternate habitats, depending on season or life stage. Theory predicts that individuals should migrate as soon as maximum profitability shifts between habitats. However, in differential migration, individuals migrate at different times for reasons that are still relatively poorly understood, though theoretical and empirical approaches have been used to test for mechanisms causing differential migration. Conflicting hypotheses, often involving either physiological barriers or tradeoffs between mortality and reproduction, can predict identical migratory timing. So far, their influence has not been disentangled in wild populations. We use a model to show that differential migration patterns can be explained solely through predation risk-growth rate tradeoffs. Based on this, we test for causes of differential migration in salmonids, which are among the most iconic migrants, covering long distances and surmounting large obstacles on their journey. We compare model output with empirical data of migratory timing in hundreds of juvenile trout, individually equipped with electronic tags. The data agrees with our predictions based on tradeoffs between predation and growth, in a system without physiological barriers. We suggest that similar tradeoffs may also drive migratory timing in other species.

Oral presentation abstracts

Ecology and Life History Traits

Environmental and anthropogenic determinants of the structure of Alpine marmot family groups

Sonja Lötscher, University of Zürich
Benedikt Schmidt, University of Zürich; Karch
Arpat Ozgul, University of Zürich

Environmental change and anthropogenic stressors increasingly affect the alpine ecosystem. One species, well-adapted to alpine ecosystems, is the Alpine marmot, which is known to be sensitive to both heat stress and human disturbance. Habitat preferences of Alpine marmots have been investigated in previous studies; however the interaction of environmental and anthropogenic factors on population dynamics have not been investigated, even though they usually act in concert. In this study, we aim to analyse the effects of environmental and anthropogenic factors, as well as the spatial social structure, on the abundance and occupancy of Alpine marmots. We surveyed a marmot population, consisting of ~119 family groups, in the Bernese Alps of Switzerland. Using a robust design approach, both presence and abundance were recorded with replication (3-5 replicates) at three specific periods during the summer 2017: in May (shortly after emergence), in July (emergence of pups) and in September (before hibernation). We analysed the data using N-mixture and occupancy models and tested how anthropogenic disturbance interacted with environmental and social factors to affect both marmot presence in a territory and family group sizes. Our results provide insight into vulnerability of this species to increased environmental and anthropogenic disturbances.

Oral presentation abstracts

Ecology and Speciation

Endosymbiosis, the original sin? How cell fusion could have evolved to mitigate mitochondrial meltdown

Anaïs Tilquin, University of Zürich

Joshua Christie, University of Zürich

Hanna Kokko, University of Zürich

Earth, approx. 2 billion years ago. Some cells we know little about underwent dramatic changes, which were to give rise to the eukaryotic lineage. Linear chromosomes, a nucleus, organelles, sex... those are some of the features common to extant eukaryotes. But in what order did they all appear in our ancestor? Here we build on a recent idea that mitochondria played a key role in the evolution of sex.

Imagine some early eukaryotes whose fitness has become dependent on functional mitochondrial symbionts, and that have so far only reproduced asexually. The absence of cell fusion means that each mitochondrial lineage is trapped within one eukaryotic lineage, and over time, separate lineages accumulate a different set of deleterious mutations. Under these premises, the merging of two eukaryotic cells, and the resulting heteroplasmy, could have restored a high fitness by allowing different mitochondrial strains to complement each other. I will present results from a model showing the conditions under which regular cell fusion could then have evolved.

Was early sex only about cytoplasmic mixing then? From there, the invention of genetic recombination could have followed, which, associated with the massive transfer of mitochondrial genes to the nucleus, finally made cytoplasmic mixing obsolete. Modern eukaryotes were born. Maybe? That is what we'll discuss.

Oral presentation abstracts

Ecology and Speciation

Ecological predictors of social organization in the Alpine silver ant

Sacha Zahnd, University of Lausanne

Jessica Purcell, University of California Riverside

Julie Lee-Yaw, University of British Columbia

Michel Chapuisat, University of Lausanne

Insect societies vary in their social organization, yet the influence of ecological factors on the maintenance of this variation remains poorly understood. In the Alpine silver ant *Formica selysi*, colonies headed by one queen (monogynous) or by several queens (polygynous) occur in the same populations. Alternative social forms are controlled by a supergene and are differing in several life-history traits. Using a niche modeling approach, we aim to unravel the ecological factors shaping the distribution of each social form. We found that elevation, vegetation cover and precipitation are the main factors shaping the distribution of social forms. Interestingly, we have found that monogynous colonies are occurring in harsher areas, less suitable for the species. This would suggest that polygynous colonies exclude monogynous ones from suitable environment. Queen reacceptance would be a great advantage for fast-growing polygynous colonies in suitable and stable habitat. In the opposite, larger monogynous queen could disperse further and occupy less suitable habitat. These results provide insights on how ecological factors help maintaining social organization polymorphism.

Oral presentation abstracts

Ecology and Speciation

Niche partitioning among individuals in natural phytoplankton communities and experimental populations

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Biodiversity and Conservation Biology, WSL

Mridul K. Thomas, Centre for Ocean Life, DTU Aqua, Technical University of Denmark

Mirela Moldoveanu, Department of Ecology, Taxonomy and Nature Conservation, Institute of Biology Bucharest, Romanian Academy

Marta Reyes, Department of Aquatic Ecology, Eawag

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Cellular traits – which determine responses to the abiotic and biotic environment - may help us rigorously link microbial diversity and ecosystem properties. Using phytoplankton data obtained from 28 lakes sampled at different spatial and temporal scales, we found that the diversity in individual-level morpho-physiological traits strongly improved our ability to predict community resource-use and biomass yield compared to taxonomic richness and evenness. The regularity in distribution of individual cells/colonies within trait space was the strongest predictor, exhibiting a robust negative relationship across scales. We hypothesized that this negative relationship can be driven by resource limitation, which induces niche partitioning among individuals through phenotypic plasticity or selection while decreasing total productivity at the same time. We tested this hypothesis by growing two phytoplankton species (*Pseudokirchneriella subcapitata* and *Microcystis aeruginosa*) in monocultures and mixed communities under six light intensity regimes. Low light levels, as hypothesised, induced an increase in even distribution of pigment-related traits. Our results provide experimental evidence of how resource limitation can shape phenotypes in a competitive environment and may help understand how to link physiology to ecosystem-scale processes. This could improve our ability to forecast changes in ecosystem properties across environmental gradients.

Oral presentation abstracts

Ecology and Speciation

Ecological opportunity predicts charr diversity of Greenlandic lakes

Carmela Doenz, University of Bern & Eawag
Catherine E. Wagner, University of Wyoming
Jakob Brodersen, University of Bern & Eawag
Ole Seehausen, University of Bern & Eawag

Imagine a new environment with a variety of ecological niches appears and is colonized by a species that, by adapting to these niches, rapidly evolves into many new species. This process, known as adaptive radiation, relies on the availability of ecological niches (ecological opportunity) as well as on the intrinsic potential of the colonizing taxon to undergo adaptive diversification and speciation. However, only few studies have explored the relationship between these two factors and the diversity accumulating during adaptive radiation. Here, we assess how proxies of ecological opportunity relate to ecomorph diversity of Arctic charr (*Salvelinus* spp.) in postglacial lakes in Greenland. Using morphological, neutral genetic and ecological data, we identify up to six sympatric charr ecomorphs per lake. We find that ecological opportunity provided by a lake is positively related to charr ecomorph diversity and also predicts whether a given ecomorph occurs within a lake or not. Our data suggest that the combination of stepwise incidence functions for different ecomorphs produces the gradual relationship of ecomorph diversity and ecological opportunity we observe. We discuss our findings in the context of evolutionary community assembly through adaptive radiation.

Oral presentation abstracts

Ecosystems

Community evolution increases the stability of grassland plant communities during unperturbed and perturbed states

Sofia van Moorsel, University of Zurich

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An increase in extreme weather events demands a deep understanding of how communities respond to environmental perturbations. We know that biodiversity increases stability in grassland plant communities during unperturbed states and in response to environmental perturbations such as droughts and floods. We hypothesized that not only plant diversity but also community history can buffer plant communities and consequently increase ecosystem stability. Using a long-term biodiversity experiment with 52 species growing in four species diversity levels we tested both the influence of plant community history and the influence of soil community history on the stability of plant community productivity over four years and resistance, resilience and recovery in response to a flood in spring 2013. We grew plant communities with eight years of co-occurrence in the field adjacent to identical communities lacking such a common history. The communities were planted in native soil, neutral soil and sterilized soil containing a native soil inoculum. Selected plant communities were more stable over time, especially in low diversity plots, and recovered better from the flooding event. Native soil treatments did stabilize productivity during unperturbed states but did not further increase resistance to the flood. Our results suggest that community evolution might play an important role in mediating ecosystem stability, which has implications on ecosystem management and conservation strategies.

Oral presentation abstracts

Ecosystems

Biodiversity increases and decreases ecosystem stability

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Losses and gains in species diversity affect ecological stability and the sustainability of ecosystem processes and services. Experiments and models reveal positive, negative, and no effects of diversity on individual components of stability, such as temporal variability, resistance, and resilience. Poorly appreciated, however, is how these stability components co-vary, and therefore how “overall ecosystem stability” (akin to ecosystem multifunctionality) is affected by diversity. We observed how stability responded to diversity in a very large experiment involving 720 micro-ecosystems. Increased species richness increased temporal stability but decreased resistance to temperature differences. Thus two stability components traded-off along the diversity gradient. Previous biodiversity manipulation studies rarely reported such a tradeoff. Integrating these findings with a new generalisation of ecosystem multifunctionality revealed the plausibility of an otherwise elusive hump-shaped effect of diversity on overall ecosystem stability. That is, biodiversity increases overall ecosystem stability when biodiversity is low, and decreases it when biodiversity is high. This generalised approach to ecosystem multifunctionality and overall ecosystem stability could be critical for translation of science into policy-relevant information, and can fundamentally transform perceived effects of diversity on ecological stability.

Oral presentation abstracts

Ecosystems

Are the plant communities of biodiversity experiments representative of naturally assembled ecosystems?

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Biodiversity-ecosystem function (BEF) experiments were originally designed to test the hypothesis that the diversity of an ecosystem affects its functioning. While their results have broadly supported this hypothesis, their wider relevance and capacity to inform policy and practice has been extensively debated. Here, we performed a comparative analysis of grassland plant communities from two large-scale, long-term projects: the Jena Experiment (a grassland BEF experiment with 82 plots) and the naturally assembled Biodiversity Exploratories grasslands (150 plots in three regions).

For both datasets we combined plant species cover data with information on phylogenetic distances and functional traits. Using principal components analysis, we assessed the multidimensional similarity of the communities based on several properties, including measures of phylogenetic and functional diversity and community weighted means of plant traits. Experimental communities covered a much larger area of multivariate space, despite the far greater geographic extent of the 'real-world' grasslands. However, there was also overlap between the two datasets, indicating that some Jena plots possess properties comparable to natural grasslands. These results suggest that diversity experiments simulate a very wide range of changes in the functional properties of vegetation, but that many of these changes are not currently observed in natural and semi-natural ecosystems.

Oral presentation abstracts

Ecosystems

The PaNDiv Experiment: individual and interactive effects of diversity, functional composition and nitrogen on grassland ecosystem function

Noémie Pichon, University of Bern
Seraina Cappelli, University of Bern
Eric Allan, University of Bern

Nitrogen enrichment is a major global change driver. Higher nitrogen inputs lead to increased plant biomass production but also to the loss of species diversity, shifts in functional composition and altered multitrophic interactions. Whilst many of these effects have been studied in isolation, e.g. the impact of diversity loss, their relative importance in affecting ecosystem function is not well known. To investigate the importance of these different direct and indirect effects of nitrogen a grassland field experiment was established to factorially manipulate nitrogen enrichment, species diversity, functional composition as well as presence of foliar fungal pathogens. The experiment, located near Bern in Switzerland, comprises 336 plots of 2x2m sown with different numbers and compositions of 20 common grassland herbs and grasses. Impacts on ecosystem functioning are assessed by evaluating changes in carbon and nitrogen cycles, biomass production and litter decomposition. Preliminary results indicate that diverse communities established faster (had lower abundance of weeds) and had higher rates of soil respiration even in the first season. Fungal pathogen exclusion also increased establishment success. These results suggest that indirect effects of nitrogen enrichment, via diversity loss and altered multitrophic interactions, are likely to have large effects on grassland ecosystem functioning.

Oral presentation abstracts

Evolutionary Genetics

Selfish manipulation of migration propensity in house mice

Jan-Niklas Runge, University of Zurich

Anna Lindholm, University of Zurich

Cooperation within the genome is essential to life, but open to exploitation. Selfish genetic elements (SGE) parasitise this cooperation by increasing their transmission to the detriment of the rest of the genome and organism. The resulting conflict can initiate an arms race between the SGE and the rest of the genome. For example, male meiotic drivers, a type of SGE, manipulate spermatogenesis and increase the transmission of driver-carrying sperm by harming the rest. As a consequence, they perform poorly in sperm competition. The rest of the genome can be selected to increase sperm competition via behavioural changes. But how does the SGE respond to this selective pressure? We hypothesized that a male meiotic driver in house mice, the *t* haplotype, was selected to increase migration propensity in its host to enhance the probability that it emigrates from unsuitable, dense populations where sperm competition is high. It could then rapidly benefit due to its transmission advantage in suitable, small, populations. We tested this by setting up agent-based simulations of the *t*'s evolution. We show that an increased migration propensity can be selected in the *t* and that this trait can prevent the *t* from going extinct. Furthermore, we present early insights from experimental populations, aimed at replicating a long-term study population from which *t*-carriers were more likely to emigrate than wildtype mice.

Oral presentation abstracts

Evolutionary Genetics

The Rocky Mountains as a dispersal barrier between barn owl (*Tyto alba*) populations in North America

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Geological barriers within a species range play a key role in shaping patterns of genetic variation by restricting gene flow. Mountain ranges are particularly imposing barriers responsible for creating genetic differentiation across multiple taxa, from small amphibians to large mammals and birds. Here, we examined the population structure of North American barn owls (*Tyto alba*) and investigated whether the Rocky Mountains influence gene flow at the continental scale. We collected 292 samples covering the species range, genotyped them at 20 microsatellite markers and sequenced one mitochondrial gene. Additionally, we obtained range-wide recapture data of wild individuals. Landscape genetics tools and spatial analyses were used to investigate range-wide patterns of structure and identify barriers to gene flow and dispersal. We found faint overall genetic structure, which is consistent with barn owl's high mobility across its continuous range. Nonetheless, we identified two distinct genetic lineages on the western and eastern regions of the Rocky Mountains with a contact-point through a narrow southern pass. Likewise, we found practically no exchange of individuals between the two regions. The Rockies appear to significantly isolate the populations in the west, which display lower genetic diversity than their counterparts to the east. Our study supports the hypothesis that regional landscape barriers can shape gene flow and population structure even in highly mobile organisms.

Oral presentation abstracts

Evolutionary Genetics

A population-level invasion by transposable elements in a fungal pathogen

Ursula Oggenfuss, University of Neuchâtel

Daniel Croll, University of Neuchâtel

Transposable elements (TEs) are important drivers of genome evolution and can impact the expression of phenotypic traits. TEs spread by insertion into novel genomic locations. In the fungal pathogen *Zymoseptoria tritici*, insertion of TEs contributed to the evolution of fungicide resistance and the surmounting of host immunity. These impacts of TEs on phenotypic traits point to a key role of TEs in adaptive evolution. However, the population-level context of TE dynamics is poorly understood. To address this, we analysed whole genome sequences of 245 fungal strains across five populations of *Z. tritici*. We used mapped reads to identify genome-wide TE insertion and deletion sites. We identified a total of 2'161 sites in the genome that were polymorphic for the presence or absence of a TE. A significant excess in rare insertions compared to neutral polymorphism was found, showing that TE insertions were overall under strong negative selection. We focused on a pair of populations that was collected in the same field at an interval of 25 years. Neutral markers showed that the populations diverged only very little by genetic drift, but a small subset of TE loci swept to near complete fixation. These rapid frequency changes driven by strong positive selection point to adaptive roles of individual TE insertions. Our study shows that TE invasion dynamics at the population scale could serve as a model to recapitulate TE-driven genome evolution over deeper evolutionary timescales.

Oral presentation abstracts

Evolutionary Genetics

The effect of parasite infection on the recombination rate of the yellow fever mosquito *Aedes aegypti*

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Lea Moesch, ETH Zurich

Nathalie Bovet, University of Neuchâtel

Anouk Sarr, University of Neuchâtel

Jacob Koella, University of Neuchâtel

The Red Queen hypothesis suggests that host-parasite interaction may select for sexual reproduction and meiotic recombination in the host's population. If common genotypes are preferentially attacked by parasites, hosts will gain an advantage by producing offspring with rare and novel genotypes, for these will be temporarily free from infections. Sexual reproduction and meiotic recombination generate unfamiliar genetic combinations and thus help hosts to respond to parasite-induced selection. We used the yellow fever mosquito *Aedes aegypti* to test whether the proportion of recombinant offspring increased plastically after the infection of the microsporidian parasite *Vavraia culicis*. We choose 6 microsatellites distributed over the chromosome 3 of *Aedes aegypti* to obtain the genetic profiles of the infected and uninfected females and of their relative descendants, and we measured the recombination fraction. We found that the infected females increase their recombination rate compared to the uninfected ones. This was particularly evident at intermediate genetic distances between couples of microsatellites, whereas at short and long genetic distances where the recombination is respectively minimal or maximal by nature, the effect was negligible. These results, in accordance with the Red Queen hypothesis, show the ability of the host to diversify their offspring in response to parasite's infection by actively distorting the recombination rate in only one generation.

Oral presentation abstracts

Population Genetics

The dynamics of expansion load and recovery during species range shifts

Gilbert Kimberly, University of Bern
Stephan Peischl, University of Bern
Laurent Excoffier, University of Bern

Populations undergoing spatial range expansions are subject to gene surfing, which is known to contribute to maladaptive expansion load. During a standard range expansion, populations at the expanding front experience reduced efficacy of selection due to small effective population size and repeated founder events as they continue to colonize new habitat. This demographic process creates surfing of deleterious variants that lead to significant reductions in fitness. However, after an expansion and once population size recovers, migration from the core of a species range combined with more efficient selection lead to recovery from expansion load. We investigate similar demographic process, a range shift, where an expanding front occurs ahead of a receding trailing edge. We hypothesize that these shifts are more common for specialist species that track specific environments over space as climate or other environmental conditions change. As this constant-width population moves over space, expansion load accumulates at the front, and extinction at the trailing edge eliminates beneficial diversity that would persist in a standard range expansion. Through simulation, we show that this demographic process can lead to further fitness reductions than a standard range expansion, and furthermore may prevent recovery and leave populations in a state of reduced fitness and thus more prone to extinction from any stochastic forces that may threaten their long-term persistence.

Oral presentation abstracts

Population Genetics

Social polymorphism is favoured by the co-evolution of dispersal with social behaviour

Charles Mullon, University of Lausanne

Laurent Keller, University of Lausanne

Laurent Lehmann, University of Lausanne

Dispersal determines gene flow among groups in a population and so plays a major role in many ecological and evolutionary processes. Because gene flow shapes kin structure, dispersal is important to the evolution of social behaviours that influence reproduction within groups. Conversely, dispersal depends on kin structure and social behaviour. Dispersal and social behaviour therefore co-evolve but the nature and consequences of this interplay are not well understood. Here, we show that it readily leads to the emergence of two social morphs: a sessile, benevolent morph expressed by individuals who tend to increase the reproduction of others within their group relative to their own; and a dispersive, self-serving morph expressed by individuals who tend to increase their own reproduction. This social polymorphism arises due to a positive linkage between the loci responsible for dispersal and social behaviour, leading to benevolent individuals preferentially interacting with relatives and self-serving individuals with non-relatives. We find that this linkage is favoured under a large spectrum of conditions, suggesting that associations between dispersal and other social traits should be common in nature. In line with this prediction, dispersers across a wide range of organisms have been reported to differ in their social tendencies from non-dispersers.

Oral presentation abstracts

Population Genetics

Blockwise Site Frequency Spectra for Inferring Complex Population Histories and Recombination

Champak Beeravolu Reddy, University of Zurich
Michael J. Hickerson, The City College of New York
Laurent A.F. Frantz, Queen Mary University of London
Konrad Lohse, University of Edinburgh

We introduce ABLE (Approximate Blockwise Likelihood Estimation), a novel composite likelihood framework based on a recently introduced summary of sequence variation: the blockwise site frequency spectrum (bSFS). This simulation-based framework uses the frequencies of bSFS configurations to jointly model demographic history and recombination and is explicitly designed to make inference using multiple whole genomes or genome-wide multi-locus data (e.g. RADSeq) catering to the needs of researchers studying model or non-model organisms respectively. The flexible nature of our method further allows for arbitrarily complex population histories using unphased and unpolarized whole genome sequences. In silico experiments demonstrate accurate parameter estimates across a range of divergence models with increasing complexity, and as a proof of principle, we infer the demographic history of the two main species of orangutan from multiple genome sequences (over 160 Mbp in length) from each species. Our results indicate that the two orangutan species split approximately 650-950 thousand years ago but experienced a pulse of secondary contact much more recently, most likely during a period of low sea-level South East Asia (~300,000 years ago). Unlike previous analyses we can reject a history of continuous gene flow and co-estimate genome-wide recombination. ABLE is available for download at <https://github.com/champost/ABLE>.

Oral presentation abstracts

Population Genetics

Origin of genetic diversity in an Amazonian fish and how to belong to a same population despite being separated by a strong environmental barrier

Luiz Jardim de Queiroz, University of Geneva

Juan I. Montoya-Burgos, University of Geneva

Understanding the processes that give rise to genetic diversity in the Amazon is challenging due to the vast scale, the environmental richness and the outstanding biodiversity. We addressed this issue by determining the genetic structure of the Amazonian fish *Triportheus albus* and assessing the role played by multiple structuring factors. The results revealed a strong structuration with three geographical groups. Two populations are found in Andean-born rivers (whitewaters), including the Amazon main course. The third population is spread only in isolated black/clearwater rivers flowing into the whitewaters of the Lower Amazon. A db-RDA identified, for the first time, that distance, topography, water colour, floodplain size and forest composition have played a role on the structuration of *T. albus*. Variance partitioning tests quantified the relative importance of the explanatory factors. The multifactorial processes highlighted here may account for the high speciation rate characterising the Amazonia. But how do fishes inhabiting disjoint black/clearwater rivers belong to a same population while separated by the whitewater population of the Lower Amazon's main course? We propose a climatic explanation in which dry periods of the Pleistocene triggered a disconnection between the Upper and the Lower Amazon. Population allopatric divergence would have been reinforced by ecological adaptation to the whitewaters vs. black/clearwater in the Upper and Lower Amazon, respectively.

Oral presentation abstracts

Population Genetics

Detecting selection from linked sites using an F-model

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Christoph Leuenberger, University of Fribourg

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Daniel Wegmann, University of Fribourg & SIB

Allele frequencies vary across populations and loci, even in the presence of migration. While most differences may be due to genetic drift, divergent selection will further increase differentiation at some loci. Identifying those is key in studying local adaptation, but remains statistically challenging. A particularly elegant way to describe allele frequency differences among populations connected by migration is the F-model, which measures differences in allele frequencies by population specific F_{st} coefficients. This model readily accounts for multiple evolutionary forces by partitioning F_{st} coefficients into locus and population specific components reflecting selection and drift, respectively. Here we present an extension of this model to linked loci by means of a hidden Markov model (HMM) that characterizes the effect of selection on linked markers through correlations in the locus specific component along the genome. Using extensive simulations we show that our method has increased statistical power compared to previous implementations that assume sites to be independent. We finally evidence selection in the human genome by applying our method to data from the 1000 Genomes Project.

Oral presentation abstracts

Sex and Life History

Can sexual dimorphism evolve because of natural selection?

Xiang-Yi Li, University of Zürich

Hanna Kokko, University of Zürich

Sexes often differ far more clearly in secondary sexual characteristics than in traits that appear naturally selected. Since species coexistence is facilitated by niche differences, the rarity of analogous within-species differences (intersexual niche partitioning) requires an explanation. We show that two spatial factors are crucial in the evolution of sex-specific resource use. First, mating competition often occurs over local spatial scales. If mating groups are moderately or very large, males are not selected to save resources for females who they are unlikely to mate with (the opposite, "gentlemanly" solution is possible under monogamy). Second, multiple resource types can promote the evolution of dimorphism, but concomitant spatial variation can cancel this effect if only one sex can thrive in some sites. Spatial variation can, however, lead to sexually dimorphic trait polymorphism: assuming stronger reproductive competition in males than in females, we predict males to be more often polymorphic in resource use.

Oral presentation abstracts

Sex and Life History

Two types of resistance against a major wheat disease *Septoria Tritici* Blotch

Petteri Karisto, ETH Zürich

Alexey Mikaberidze, ETH Zürich

Septoria tritici blotch (STB) caused by fungus *Zymoseptoria tritici* is a major disease of wheat in Europe. Breeding for quantitative resistance promises to lead to more durable disease control but is limited by difficulties in measuring quantitative differences between cultivars in a reproducible manner. We used automated image analysis on a collection of 21 420 leaves from 335 elite European winter wheat cultivars naturally infected by a diverse local population of *Zymoseptoria tritici*. We obtained precise, objective and reproducible quantitative measures of conditional STB intensity that allowed us to separate resistance affecting host damage from resistance affecting pathogen reproduction. The cultivar rankings differed between the two measures, indicating that the two types of resistance should be considered separately in breeding programs. The different forms of resistance are under separate genetic control, enabling them to be recombined to form new cultivars that are highly resistant to STB. We showed that measures of pathogen reproduction early in the season were the best predictors of host damage late in the season, illustrating the importance of breeding for resistance against pathogen reproduction in order to suppress epidemics and minimize yield losses caused by STB. These data can already be used by breeding programs to choose wheat cultivars that are broadly resistant to naturally diverse *Z. tritici* populations according to the different classes of resistance.

Oral presentation abstracts

Sex and Life History

Virus spillover from European honey bees (*Apis mellifera*) to ants (*Lasius niger*)

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Orlando Yañez, Institute of Bee Health, University of Bern

Nor Chejanovsky, Agricultural Research Organization, the Volcani Center, Israel

Peter Neumann, Institute of Bee Health, University of Bern; Swiss Bee Research Centre, Agroscope

Virus spillover from managed honey bees to wild insects can occur frequently and may contribute to population decline of the latter. Understanding the pathways of viruses and their impact seems therefore critical to mitigate potential adverse effects on wild populations. In this regard, ants have mostly been neglected in scientific research so far. Here, we used a laboratory feeding experiment to test whether the black garden ant, *Lasius niger*, is an alternative host of the honey bee Acute Bee Paralysis Virus (ABPV). Adult ants in 20 queenright colonies were fed with either ABPV infected honey bee pupae or with non-infected drosophila. After 10 weeks adult workers and queens were analysed with standard qPCR and an ABPV minus-strand specific PCR for ABPV infection. In a follow up experiment new colonies received again either infected or non-infected food and after 12 weeks they were tested with a behavioural essay. Our results show that virus-fed *L. niger* can carry ABPV and further suggest that the virus is able to replicate in this ant. Clinical symptoms of ABPV infection were impaired locomotion ability and significantly decreased movement speed of infected ants compared to non-infected controls. The results suggest that *L. niger* is an alternative host of ABPV and that foodborne transmission is the underlying acting spillover mechanism. This study contributes to our understanding of virus transmission pathways and the possible impact of infections on alternative hosts.

Oral presentation abstracts

Sex and Life History

Competition of two *Borrelia* strains inside the rodent host and the tick vector

Dolores Genné Vizcardo, University of Neuchâtel

Maarten J. Voordouw, University of Neuchâtel

Anouk Sarr, University of Neuchâtel

Vector-borne pathogens often establish mixed infections inside their vertebrate host as well as in their arthropod vector. Studies on interactions between strains have typically focused on the vertebrate host. Here we used two different strains of the Lyme disease pathogen, the spirochete bacterium *Borrelia afzelii*, to investigate the interactions of mixed strain infections inside both the rodent host and the tick vector, *Ixodes ricinus*. Mice were infected with either one strain or co-infected with both strains, and were subsequently infested with larval ticks. The engorged larval ticks were allowed to molt into nymphs, the most relevant stage for the epidemiology of Lyme disease. We used qPCR assays to determine the host-to-tick transmission success of each strain and the spirochete load of each strain inside the nymphs. The transmission rate of one of the strains was reduced in the co-infection treatment compared to the single strain infection treatment. For both strains, we found that their spirochete load was reduced by 50% by the presence of the co-infecting strain. The present study therefore demonstrates that *Borrelia* strains compete inside both the rodent host and the tick vector. Future studies should investigate whether this competition influences the tick-to-host transmission success of each strain.

Oral presentation abstracts

Sex and Life History

There's a predator around, run! Maternal effects through eggs affect offspring growth and anti-predator responses

Sakshi Sakshi Sharda, University of Bern

Matthias Erb, University of Bern

Barbara Taborsky, University of Bern

Predator induced maternal effects are known in many animal taxa and shape offspring behaviour and life history responses such as growth. However the physiological mechanisms underpinning the above phenotypic changes in offspring are largely unresolved. Further, it is unclear which traits are influenced by maternal effects and when during offspring life these traits are expressed. To understand the above, we performed an integrative study linking predator-induced maternal effects on egg composition with offspring gene expression, growth and anti-predator behaviour. We exposed pairs of the cooperatively-breeding cichlid *Neolamprologus pulcher* to visual and olfactory cues of its most dangerous natural predator, or to no-predator cues. Predator-exposed mothers laid heavier eggs with higher net protein content, indicating that mothers invest more in offspring quality under predation threat. However, fry from "no-predator" parents had a higher expression of insulin like growth factor-1 gene, which might have boosted growth to compensate for their initial size disadvantage, owing to smaller eggs. Remarkably, offspring from predator-exposed mothers showed faster startle responses implicating a role of maternal effects on offspring neural development. Predator offspring were also more risk-averse. Our results suggest that egg-derived maternal effects might exert effects on offspring phenotypes, which alter their organisation at molecular and neural levels.

Oral presentation abstracts

Sex and Life History

How is female mating choice impacted by presence of pathogens ?

Patrick Joye, University of Lausanne

One of the main theories concerning the potential benefits of male choice to females is based on male resistance to pathogens. Male attractiveness is proposed to reflect the individual's condition, and the condition is thought to be negatively affected by pathogens and parasites, making males less attractive. According to the theory, by choosing healthy males, females will gain indirect benefit by transmitting these resistance genes to their offspring. However, there are very few empirical data to support this theory. In our study, we tested if/how presence and absence of pathogens (*Pseudomonas entomophila*) and male resistance would influence female mating choice, and if this choice can impact offspring resistance in *Drosophila melanogaster* flies. When the choice is made in presence of pathogens, we found that female choose more resistant males, and yet have a more resistant offspring. Interestingly, the choice was reversed when made in the absence of pathogens, and offspring of chosen males were less resistant. This study brings highlights on how pathogens might act as an important factor influencing sexual selection, and on how genetic variation in males is maintained despite a one-sided female choice.

Oral presentation abstracts

Sex and Life History

Adaptation to juvenile malnutrition: Trade-off with adult performances

Cindy Dupuis, University of Lausanne

Berra Erkosar, University of Lausanne

Tadeusz Kawecki, University of Lausanne

Many organisms face periods of food shortage. Chronic malnutrition is likely to have a strong impact on juveniles, as they have to acquire enough nutrients for growth. What potential is there for adaptation to early-life malnutrition, and through which processes? We address these questions using experimental evolution in *Drosophila melanogaster*. For over 200 generations, we maintained several *drosophila* populations on a poor larval diet and placed them back on normal food as adults to specifically target juvenile malnutrition. Our selection regime rapidly led to adaptation to poor larval diet: selected lines show higher egg-to adult survival and grow faster on poor food than control lines. This higher tolerance is partly explained by an improved ability of larvae to accumulate fat stores and use them in the metamorphosis step. However, this benefit does not come without a cost: selecting for traits beneficial in larvae has had detrimental effects on several life-history traits, but at later life stages: selected adults have become smaller and more susceptible to starvation. We have evidence that many metabolic processes differ between selected and control adults, which could explain the observed trade-off. Future efforts will focus on further characterization of larval adaptation and investigating whether other adults traits (fecundity, stress resistance) were affected by selection.

Oral presentation abstracts

Systematics and Macroevolution

High-throughput biomonitoring of marine ecosystems with eDNA: supervised machine learning for the building of robust predictive models.

Tristan Cordier, University of Geneva

Jan Pawlowski, University of Geneva

Monitoring natural resources and ecosystem services is of prime importance for the sustainable development of human societies. Environmental impacts of human activities in marine ecosystems, such as aquaculture, oil drilling or mining operations, are traditionally assessed through benthic biodiversity surveys. This involves the sorting and the taxonomic identification of thousands of macroinvertebrates specimens, which is time consuming and taxonomic-expertise demanding. The development of high-throughput DNA sequencing has paved the way toward fast and objective description of biological communities. However, usually more than half of eDNA sequences remain unassigned or belong to taxa of unknown ecology, which prevent their use for inferring the ecological quality status of a sample. We recently showed that supervised machine learning (SML) proved efficient for the building of robust predictive models from eDNA metabarcoding data, regardless of the taxonomic assignments of the sequences. This allows to use almost all the sequences of a dataset, constituting a more holistic approach to infer the ecological quality status. Combining eDNA high-throughput sequencing and SML holds the potential to overcome the limitations of macroinvertebrates inventories. We will present recent results and future directions toward fast and accurate biomonitoring of marine environments, and discuss how such framework can be used in any other ecosystem that is subject to ecological disturbance.

Oral presentation abstracts

Systematics and Macroevolution

The role of migration in speciation: linking micro and macroevolution

Pablo Duchon, University of Lausanne

The process of speciation is of key importance in evolutionary biology because it shapes overall macroevolutionary patterns. Still, any speciation process starts at the microevolutionary level, for instance, when two diverging populations drift towards different phenotypic optima. The speed at which these optima are reached is controlled by 1) the selection strength, which pushes a mean trait towards an optimum, and 2) ongoing migration that pulls the mean phenotype away from that optimum. Traditionally, phenotypic evolution with selection has been modelled by Ornstein-Uhlenbeck (OU) processes at the macroevolutionary level, but these models have ignored the role of migration within species. Although the use of OU processes at the macroevolutionary scale has been criticised, OU-based inference is strong enough to detect phenotypic evolution at a microevolutionary (or ecological) time scale. Here, our goal is to conciliate the processes of micro and macroevolution by modelling migration during speciation. More precisely, we introduce an OU model where migration happens between two sub-populations and this migration decreases over time as it happens during speciation. We then use this model to study the evolution of trait means along a phylogeny, as well as the way phenotypic disparity between species changes with successive epochs. We find that ignoring the effect of migration in sampled time-series data leads to a significant underestimation of the selective forces acting upon our data. We further introduce a method to jointly estimate selection and migration from time-series data.

Oral presentation abstracts

Systematics and Macroevolution

A DNA barcode library for Swiss diurnal Lepidoptera: Implications for species identification, systematics and conservation

Jessica Litman, Muséum d'histoire naturelle de Neuchâtel
Yannick Chittaro, Centre Suisse de Cartographie de la Faune
Stefan Birrer, Hintermann & Weber
Sofia Wyler, Université de Genève
Yves Gonseth, Centre Suisse de Cartographie de la Faune

Switzerland is home to approximately 226 species of diurnal Lepidoptera (Rhopalocera and Zygaenidae). These species are the focus of multiple national inventories, including Red Lists and other biodiversity monitoring projects. They are also particularly useful for assessing the quality of ecosystems, as well as for evaluating the impact of climate change and habitat alteration on insect communities. While the distribution, behavior and ecology of these species is relatively well explored, their genetic diversity is less well documented. The SwissBOL (Swiss Barcode of Life) Butterfly project was thus launched to obtain baseline genetic data for Swiss diurnal Lepidoptera, to understand the geographical distribution of this diversity and to ultimately use this data to hone conservation strategies. We obtained approximately 800 sequences for over 200 species of diurnal butterflies sampled across Switzerland and used these sequences to evaluate the utility of the DNA barcode as a tool for species identification, highlighting cryptic diversity and clarifying species and sub-species boundaries in groups that remain difficult to evaluate using morphology alone. We examine Swiss butterfly barcodes in the context of existing European sequences to assess patterns of genetic diversity on a continental scale and explore how understanding patterns of genetic diversity can be used to fine-tune conservation measures.

Oral presentation abstracts

Systematics and Macroevolution

Untangling diversity and disparity in the macroevolutionary history of the cycadales

Mario Coiro, University of Zurich

Hans Peter Linder, University of Zurich

The evolution of species diversity as well as its relationship with morphological disparity remain an open topic of despite decades of research. The debate is exacerbated by the seemingly incompatible types of evidence commonly used for inferring changes in diversity and disparity. Indeed, phylogenies based on molecular data are now routinely used to infer the patterns of diversification and consequently the origin of species richness, whereas fossil data are used to infer trajectories of disparity mostly through time. The development of methods that allow the integration of fossil data in a molecular phylogenetic framework, such as the fossilized birth-death prior for dated trees, could help to bridge the chasm between fossil and molecular data, and disentangle the relationship between diversity and disparity. Here we show the potential of these methods in a case study on the Cycadales, a group with a rich but poorly understood fossil record. We inferred a dated phylogeny based on 237 extant (DNA and morphology) and 68 fossil cycads and use this tree to test both the older “living fossil” and the more recent “synchronous radiation” hypothesis. The evolutionary dynamics of leaf disparity and species diversity, evident from this tree, are inconsistent with both hypotheses. Generally, disparity and diversity are asynchronous; and the whole pattern of diversifications is shaped by heterogeneous processes.

Poster presentation abstracts

Poster Presentations Abstract Book

Bayesian estimation of partial population continuity using spatially explicit simulations

Jeremy Rio, University of Geneva

Nuno Silva, University of Geneva

Mathias Currat, University of Geneva

Advances in sequencing technologies allow retrieving ancient DNA (aDNA) from fossils to provide snapshots of genomic diversity in past populations. Models used for the exploration of genetic relationships between samples from different periods usually consider a panmictic population and thus do not consider the spatiotemporal dynamics of genes due to migration. Here, we present a spatially explicit approach, simulating genomic diversity using a modified version of the program SPLATCHE2 and samples of different ages and locations, that takes into account population structure and migration over time. We apply our new approach to two ancient genomes from central Europe to investigate the genetic consequences of the change in lifestyle that occurred during the Neolithic transition in this region. In order to understand if this change was accompanied by a population replacement in central Europe, we estimated the amount of genetic continuity between Paleolithic hunter-gatherers and Neolithic farmers. While previous approaches rejected the hypothesis of full population continuity, our method goes one step forward by estimating the most probable genetic contribution of hunter-gatherers from different parts of Europe to the final Neolithic population in central Europe. Our new approach constitutes a useful tool for the analysis of aDNA datasets, applicable to many species and research contexts.

Poster presentation abstracts

Poster N°2

EnhanceR, Research IT Support for the Swiss Research Community

Alex Upton, ETH Zurich

EnhanceR Project Consortium, Various (inc. UZH, ETHZ, UniBas, FMI, EPFL, SIB, UniBe, Hes-so)

Research presents unique IT challenges. Supporting researchers in meeting these challenges has led to the creation of specialist units to provide Research IT support, allowing researchers to concentrate on their core tasks and accelerating time to results. Through the EnhanceR project, these units are federated into a national cooperative Research IT support community to provide support, transfer knowledge and build skills and capacities in the Swiss research academic sector.

EnhanceR is the follow-up to the successful eSCT project, which assisted a wide number of researchers across Switzerland through the delivery of over 50 support projects. These ranged from the development of a scalable neuroscience imaging analysis pipeline, to the benchmarking of sequencing alignment tools, to the creation of a multi-institute resource-sharing platform that now has over 4,000 users.

Here, we outline the services that EnhanceR offers researchers, as well as two examples of previous support projects. Firstly, we detail the development of a scalable imaging analysis pipeline that aided researchers at the Neural Circuit Dynamics lab at the University of Zurich. Secondly, we present the development of a technology stack to run the same workflow in different Swiss HPC clusters, aimed at projects with sensitive and confidential data where code has to move to the data. Finally, we present an overview of the project consortium, providing details on how interested researchers can access support.

Poster presentation abstracts

Poster N°3

Grassland ecological quality: how do indicator plant species predict invertebrate diversity?

Maria Weinrich, University of Bern
Raphaël Arlettaz, University of Bern
Jean-Yves Humbert, University of Bern

Today, extensively managed meadows registered under Swiss agri-environment schemes (AES) represent around 8% of the Swiss farmland. In addition to the input-based payments, farmers can get output-based financial reward if their AES meadow reaches a certain ecological quality. The quality of the meadow is evaluated with an assessment key that is based on the presence/absence of indicator plant species.

The aim of this study was to determine if the number of indicator plant species predicts well the invertebrate community (species richness and abundance) inhabiting the meadow. The assessment key was applied in 47 extensively managed AES meadows located on the Swiss Plateau and tested against the diversity of invertebrates (including butterflies, hoverflies, wild bees, spiders, parasitoid wasps, moths, orthopteran, auchenorrhyncha, rove- and ground beetles).

The results showed that invertebrate multidiversity (standardized mean diversity across all taxa) positively correlated with the number of plant indicators. Specifically, a positive correlation between herbivore diversity and number of indicator plants was found, and like hypothesized this trend was mostly driven by mono- and oligophagous pollinators. On the other hand, no correlation was found with predator species.

While the current key is a good method to assess rapidly the meadow plant and invertebrate herbivore diversity, it might need a complement if diversity of invertebrate predators wants to be taken in account.

Poster presentation abstracts

Poster N°4

Performance of PIT tags used for identification of individuals and quantification of feeding rates in Hoopoes (*Upupa epops*) in relation to chick age, feeding posture and parent gender

Noëlle Klein, University of Bern

Passive integrated transponders (PIT tags) are frequently used for research, especially in birds for identifying individuals and quantifying feeding rates. However, studies about the efficiency of this system are rare. In this study, the PIT tag performance was evaluated by testing the system on hole-breeding single-load feeders by using six Eurasian Hoopoe individuals from Central Valais in southern Switzerland. Overall, the PIT tags worked in 96.75% of all 1261 monitored events and can be considered as a good system for identifying tagged individuals. The performance of the system depended on the position of the bird relative to the antenna, the breeding phase and the sex of the bird. Only 783 out of 1261 events were identified as actual feeding events, and the system was not always triggered at exit events and doesn't work for feeding events from outside, when the chick holds its head outside. Thus, PIT tagging cannot be considered as an appropriate method for measuring incubation and feeding patterns in Hoopoes, which contradicts former predictions and studies in other bird species.

Poster presentation abstracts

Poster N°5

Molecular species diagnosis in CITES-listed *Dalbergia* precious woods: insights and implications for forensic timber identification

Simon Cramer, ETH Zurich, Institute of Integrative Biology, Plant Ecological Genetics, Zurich, Switzerland.

Sonja Hassold, ETH Zurich, Institute of Integrative Biology, Plant Ecological Genetics, Zurich, Switzerland.

Porter P. Lowry II, Missouri Botanical Garden, St Louis, MO, USA and Laboratoire de Phanérogamie, Muséum National d'Histoire Naturelle, Paris, France.

Alex Widmer, ETH Zurich, Institute of Integrative Biology, Plant Ecological Genetics, Zurich, Switzerland.

Establishment and enforcement of the CITES convention rely on correct species identifications to assess the status of exploited species, to identify individuals to be harvested, and to verify species identity declarations. Species diagnosis is challenging in many timber species due to insufficient reference collections and because identification keys often rely on flower and fruit characters, which are often absent on living specimens or logs awaiting inspection. This facilitates international trade in illegally logged and wrongly declared timber and calls for methods enabling accurate species diagnosis of standing trees and logs.

We blindly sampled Malagasy *Dalbergia* rosewood species (Fabaceae, CITES appendix II) in the field to explore whether species can be delimited using molecular markers. We then contrasted the molecular data with leaf morphological characters and evaluated the delimited units against existing taxonomic descriptions of Malagasy *Dalbergia* species. Classification analysis revealed that molecular data achieved substantially higher species-level resolution compared to leaf morphology, leading to a much lower misidentification rate.

In conclusion, molecular species delimitation and diagnosis can be used to inform taxonomic revisions and to improve morphological identification keys. This paves the way for correct species identification of reference collections and thus provides the scientific foundation for all forensic timber identification techniques.

Poster presentation abstracts

Poster N°6

The effects of handling disturbance on feeding and pattern in the European Hoopoe (*Upupa epops*)

Julia Besimo, University of Bern
Noëlle Klein, University of Bern
Alain Jacot, University of Bern
Raphaël Arlettaz, University of Bern

Conservation research often requires disturbing the species of interest. Therefore, it is crucial to investigate the effects of this disturbance and to adjust the experimental approach accordingly. In this study, handling disturbance on the European Hoopoe, an endangered bird in Switzerland, was investigated. The artificial study population is located in Central Valais, Switzerland and their population dynamics have been studied for several years. For this study, feeding performance and chick survival with or without handling disturbance were evaluated for 17 selected breeding pairs. Females and males did react differently to disturbance. Males were feeding less in terms of feeding rate and biomass while females fed more. Nevertheless, females could not compensate the poor performance of the male. In addition, the survival of the chicks was lower for nests which experienced disturbance. Thus, handling disturbance on this population should be reduced or at least delayed, so that the chicks are not in such a vulnerable stage anymore. This study showed that research induced disturbance can affect individuals negatively, which is most probably a common phenomenon.

Poster presentation abstracts

Poster N°7

Effects of habitat fragmentation on bumblebee foraging trip duration and colony fitness

Corina Maurer, University of Bern

Laura Bosco, University of Bern

Alain Jacot, University of Bern

Raphaël Arlettaz, University of Bern

Many species of wild pollinators, including bumble bees, are declining (Potts et al. 2010). Agricultural intensification with the associated habitat loss and fragmentation are among the most important drivers (Robinson & Sutherland 2002; Goulson, Lye & Darvill 2008; Potts et al. 2010). In this study, we investigated the effects of habitat fragmentation on bumblebee foraging trip duration and colony fitness by placing 40 colonies of *Bombus terrestris terrestris* in vineyard fields in Valais, Switzerland, varying in habitat amount and fragmentation. We measured foraging trip duration with RFID (radio frequency identification) technology to automatically register when the tagged bumble bees leave and enter the hive. Colony fitness was assessed by counting several nest parameters. First results show that in areas with low habitat amounts but high fragmentation degree, bumblebee colony fitness was lower in terms of colony size. On the other hand we could show a positive effect of fragmentation in areas with high habitat amounts on colony fitness, indicating that a certain heterogeneity is beneficial. Further, we could show a general positive effect of vegetation cover in vineyards on colony fitness. Based on those first results, we recommend to increase the number of vegetated vineyards up to a certain maximum in order to create a mosaic of vegetated fields interspersed by bare vineyards.

Poster presentation abstracts

Poster N°8

Plant reproductive success in highly fragmented Valais vineyard landscapes: a quasi-experimental approach

Elisabeth Klaus, University of Berne

Alain Jacot, University of Berne

Laura Bosco, University of Berne

Raphaël Arlettaz, University of Berne

The ongoing intensification of agriculture has led to landscape modifications resulting in habitat loss, degradation or fragmentation. For plant populations those processes can have severe effects mediated for instance through a reduced reproductive success. Pollinators are essential for sexually reproducing plants; hence reproduction might be limited if less pollinators visit isolated patches and less conspecific plants for pollen exchange are available. In this study, we focused on a vineyard agro-ecosystem, representing a near-binary system (vineyards with and without ground vegetation) in Valais, Switzerland. Reproductive success and pollinator visitation rate of four plant species (*Lotus corniculatus*, *Trifolium pratense*, *Centaurea jacea* and *Sinapis alba*) were studied. Potted plants were placed in vegetated vineyards with varying degrees of fragmentation and habitat amount in their surroundings. Our results for two of the four plant species suggest that in our study system habitat amount and fragmentation has no impact on plant reproductive success. However, we found that pollinator visitation rate has a positive effect on reproductive success and in turn, pollinators are positively impacted by ground vegetation. These preliminary results emphasize that for reproductive success of plant species, ground vegetation seems to be of great importance, especially for the attraction of pollinators.

Poster presentation abstracts

Poster N°9

Community development of soil nematodes during heathland restoration in the Netherlands

Benetková Petra, Charles University

Jan Frouz, Charles University

Heathlands represent an important natural and cultural heritage of the Netherlands and Natura 2000 protected habitat. However, the area of European heathlands rapidly decreased during the last 100 years due to intensified agricultural practices, massive and cheaper production of artificial fertilizers, and acidification. Therefore more heathland restoration attempts are under way nowadays. Analysis of nematode community is one of the tools for assessing maturity and complexity of the soil food web, which is important for maintaining restored habitats.

We collected up to 60 samples every year in 2011, 2013, 2014 and 2015 from experimental sites (launched in 2011) where different methods were applied in a 3 X 3 factorial experiment (acidification, liming, control x plant addition, soil addition, control); reference heathlands were sampled as well to identify the target community. We sampled both dry and wet heathlands. Nematodes were extracted and analyzed for absolute abundance, trophic groups, and genera dominance. We calculated also various indices to describe the condition of nematode community. Here we present preliminary results from these analyses.

Findings of this study may help to understand the process of soil fauna development during the primary succession on oligotrophic habitat under various moisture regimes.

Poster presentation abstracts

Poster N°10

Habitat selection of a threatened alpine bird species: building the evidence for conservation management

Arnaud Barras, Institute of Ecology and Evolution, Conservation Biology, University of Bern

Arnaud Barras, Institute of Ecology and Evolution, Conservation Biology, University of Bern

Jérémy Savioz, University of Fribourg

Raphaël Arlettaz, Institute of Ecology and Evolution, Conservation Biology, University of Bern & Swiss Ornithological Institute

Species of mountain ecosystems are expected to be particularly vulnerable to climate change in future years, with a predicted altitudinal shift of suitable environmental conditions. However, current habitat changes occurring at the ecotonal timberline zone can still mainly be attributed to land abandonment. Therefore, it is unclear which factor is mainly driving the rapid decline of the Ring Ouzel, a red-listed bird species typical of the forest limit. Information on basic ecological requirements of the species is still missing, but would prove essential to evaluate the potential contribution of these two drivers.

To identify crucial species-habitat associations, we focused on the selection of foraging grounds during the breeding period, and linked it to food availability. We therefore sampled invertebrates prey in 2014 and tracked 40 birds during the chick provisioning period using telemetry in 2015-17. Foraging birds selected soft soils with high moisture and short vegetation, with high accessibility to the ground layer. On the contrary, total arthropod biomass was positively correlated with vegetation cover and height, in particular earthworms, which constitute the main prey. These results show a likely trade-off between prey accessibility and abundance, and confirm the vulnerability of the species considering predictions of advanced snowmelt and phenology. It also suggests a negative effect of pastoral abandonment, reducing vegetation heterogeneity and prey accessibility.

Poster presentation abstracts

Poster N°11

The effect of lamp proximity to aquatic habitats on the attraction of adult aquatic insects

Claudia Blumenstein, University of Bern

Deborah Carannante, University of Bern

James Hale, University of Bern

Raphaël Arlettaz, University of Bern

The availability of cheap LED lamp technology may result in a shift in the spatial extent and quality of night time outdoor lighting. The impact of LED lamps on sensitive habitats such as streams and riparian areas is largely unknown, despite lighting often being installed close to lakes and rivers. Increasing light pollution therefore poses an additional risk for taxa such as Ephemeroptera and Trichoptera which are already threatened by water pollution and habitat degradation. Terrestrial adults of many aquatic insect species are known to be attracted by artificial lighting, yet little information is available to support applied conservation practice. To address this gap, we undertook a controlled field experiment by placing LED lamps and modified flight intercept traps at different distances from a light-naïve river. We had the following questions

- a. Is there a lighting effect on the abundance of Ephemeroptera and Trichoptera?
- b. What is the magnitude of the lighting effect?
- c. Is proximity of the lamp to the river important?
- d. Is there a river proximity threshold for impacts?

We could show that the light treatment has a significant positive effect and distance a significant negative effect on abundance of both taxa. We could show that abundance around LED lamps reduces in a non-linear manner, with distinct river-proximity thresholds. Our results could be used to directly inform lighting management along freshwater bodies to reduce ecological impacts.

Poster presentation abstracts

Poster N°12

Age and season-related distribution patterns of the bearded vulture

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Daniel Hegglin, Stiftung Pro Bartgeier

Raphaël Arlettaz, Conservation Biology Institute of Ecology & Evolution, University of Bern

Veronika Braunisch, Conservation Biology Institute of Ecology & Evolution, University of Bern

The recent increase of wind energy use in Central Europe incurs potential impacts on wildlife. Large soaring raptors, like the bearded vulture, are particularly exposed to collision risk with wind turbines as they sometimes converge in selecting fairly similar combinations of landscape and wind conditions. Considerable efforts and resources have been invested to re-instate the species in the European Alps. There exists a risk, however, that this success will be jeopardized by the sprawl of the wind parks across the alpine massif. We used a maximum entropy modelling approach to predict the potential distribution of the bearded vulture across the Swiss Alpine range using presence-only data. We identified and ranked the environmental variables most relevant for the species and tested for differences in ecological requirements between two different age classes (adults and juveniles) in both the cold and the warm season separately. We found that adults and juveniles show different habitat selection patterns in both seasons with juveniles being less specific and using a wider range, which makes them potentially more vulnerable to wind energy construction. This analysis provides a first, broad-scale overview of the species distribution across the Swiss Alps. We will now further investigate the flight altitude and movement patterns at fine spatial scale in order to identify the sites bearded vultures use most intensively at risky flight heights.

Poster presentation abstracts

Poster N°13

What drives the decomposition of organic material in urban gardens?

Simon Tresch, University of Neuchatel, Institute of Biology, Functional Ecology Laboratory
Renée-Claire Le Bayon, University of Neuchâtel, Institute of Biology, Functional Ecology Laboratory
Andrea Zanetta, University of Fribourg, Department of Biology, Ecology & Evolution
David Frey, ETHZ, Department of Environmental System Science, Institute of Terrestrial Ecosystems
Andreas Fliessbach, Research Institute of Organic Agriculture (FiBL), Department of Soil Sciences
Marco Moretti, Swiss Federal Research Institute WSL, Biodiversity and Conservation Biology

Gardens are hot spots for urban biodiversity, both above- and below-ground. They act as important refuges and stepping stones providing a wide range of ecosystem services such as carbon storage, nutrient cycle and habitat provision of many plant and animals species. They are considered important for human health and well-being and offer people the possibility to interact with nature even in highly densified urban areas. Only few studies have investigated below-ground diversity and soil functioning in urban gardens, probably due to the difficulty of access to private properties, where mutual trust is essential for monitoring biodiversity or soil functions. Consequently, little is known about the impact of gardening practices on soil biodiversity functioning. In this study, we try to disentangle fundamental processes that influence the decomposition in urban garden soils. We examine whether the species richness, abundance or functional diversity of four main decomposer taxa is responsible for decomposition of maize leaves and stems in different sized litter bags. In addition, we evaluate if urbanization gradient or soil management strategies influence decomposition or the decomposer communities. Urban densification puts gardens under pressure. Since sealed surface can no longer provide most ecosystem services, it is important to understand the many advantages that humans have of garden soils in order to preserve and maintaining them in a sustainable way.

Poster presentation abstracts

Poster N°14

From flies to goats: on-going investigations of the impact of environmental factors on the relict and endangered tree *Zelkova abelicea* (Ulmaceae) from Greece

Laurence Fazan, University of Fribourg

Dany Ghosn, Mediterranean Agronomic Institute of Chania, Greece

Chariton Kalaitzidis, Mediterranean Agronomic Institute of Chania (Greece)

Panos Vassilis Petrakis, National Agricultural Research Foundation (Greece)

Polymnia Sklavaki, Forest Directorate of Chania (Greece)

Hariklia Kargiolaki, Forest Directorate of Rethymno (Greece)

Ioannis Aspetakis, Forest Directorate of Iraklio (Greece)

Emmanouil Siligardos, Forest Directorate of Lassithi (Greece)

Gregor Kozlowski, University of Fribourg

Zelkova abelicea (Lam.) Boiss. is an endangered, relict and endemic tree species that grows only in the mountains of the island of Crete (Greece). This rare species is threatened mainly by the presence of numerous ovin and caprin flocks in its distribution range. Goats browse the tender young shoots and leaves and are responsible for keeping *Z. abelicea* individuals in a stunted and dwarfed bushy form with no possibility of fruit formation. Furthermore, although *Z. abelicea* produces huge quantity of fruit in masting events every 2-3 years, the majority of seeds were found to have no viable embryo. In 2014, a project for the conservation of *Z. abelicea* was initiated, including in situ and ex situ conservation actions and public awareness and outreach actions. In the scope of this project, selected stands containing *Z. abelicea* individuals were fenced to exclude browsing pressure and allow the stunted bushes to develop into fully-grown trees. Monitoring of the fenced areas showed that *Z. abelicea* individuals reacted positively in most fenced areas by growing fast and producing long shoots as soon as browsing was excluded. In addition, on-going research activities revealed the presence of a previously unnoticed insect forming galls on the flowers of the species and which could be a possible factor influencing seed soundness.

Poster presentation abstracts

Poster N°15

Foraging micro-habitat selection of the White-Winged Snowfinch *Montifringilla nivalis* in the Swiss Alps

Anaïs Binggeli, University of Bern

Jaime Resano-Mayor, University of Bern

Raphaël Arlettaz, University of Bern

Alpine ecosystems are threatened by a rapid warming impacting cold-adapted species with often limited possibility of dispersion. Snow is thought to be the major factor shaping food availability in spring, but has been steadily declining and is now melting earlier. This may change the phenology of the peak availability of invertebrates with consequent asynchrony with the breeding timing of many alpine birds. To understand their mechanistic link to their habitat at the time of the snow melt, we investigated the foraging habitat selection of the White-Winged Snowfinch during its breeding period. The Snowfinch is a species tied to the alpine zone and is predicted to lose most of its suitable habitat with warmer conditions. We observed 31 breeding populations in Valais in order to map the micro-habitat where they collected food and compare it to random pseudo-absence points taken in the close surrounding available habitat. Using GLMM, we found a clear selection of Snowfinches for the snow front where Tipulidae larvae develop and for patches of bare ground, very short vegetation and diverse ground cover. After the snow melt, Snowfinches were still selecting for patches of little developed vegetation, similar to that of the early season. This study showed the importance of snow in the Snowfinch breeding period but also of the vegetation and appeals to study whether a higher grazing pressure could compensate for the negative impacts of climate warming in supporting suitable habitats.

Poster presentation abstracts

Poster N°16

Grassland seed bank abundance and diversity under delayed and refuge mowing regime

Roman Roth, University of Bern

PD Dr Jean-Yves Humbert, University of Bern

Prof. Dr Raphaël Arlettaz, University of Bern

In the past 50 years agriculture intensified dramatically to meet the needs of the human population on earth. This intensification led to a drastic decrease in biodiversity and abundance of species in agricultural used land. To counteract this decline biodiversity promotion areas (BPA) were introduced in Switzerland.

This study investigated the effect of three different mowing regimes on the seed bank of BPA meadows in the Swiss lowland. The first regime followed the standard Swiss BPA regulation with a first cut not before 15 June. The second regime consisted of delaying the first possible cut to 15 July and the third in maintaining an uncut refuge area of at least 10% during mowing.

Contrary to the expectation, neither a difference in the seed abundance, species richness nor Shannon Index was detected. Similarly, the community weighted mean of the first flowering month of the plant species found in the seed banks did not differ between the mowing regimes.

Other studies on the same experiment have shown positive effects of the alternative mowing regimes (second and third) on different invertebrate groups such as butterflies and orthopterans. Nevertheless, the seed bank results corroborate the fact that no differences in the above ground plant community was found among the mowing regimes. Altogether it implies that even after 5 years there is no evidence that the tested alternative mowing regimes affect the seed production of the plants present in the meadow.

Poster presentation abstracts

Poster N°17

Endospores in paleoecology: Investigation of their origin in high mountain lakes

Mathilda Hayoz, University of Neuchatel
Christophe Paul, University of Neuchâtel
Thomas Junier, University of Neuchâtel
Sevasti Filippidou, University of Neuchâtel
Anaël Lehmann, University of Lausanne
Daniel Ariztegui, University of Geneva
Torsten Vennemann, University of Lausanne
Pilar Junier, University of Neuchâtel

Nowadays a thorough understanding of the environments' reaction in response to climatic change seems unavoidable. One way to do this is by studying past events of change and the response of biological communities to it. Several paleoecological studies have already used endospore-forming bacteria in order to reconstruct environmental history. Since endospores are able to survive for extended periods of time, the endospore seed bank community might reflect the evolution of these sites. However, for this approach to be validly used, the autochthonous origin of the endospore-forming community needs to be demonstrated. In this study we explore the origin of endospores in two alpine lakes located in Grisons, Switzerland (Jöri lakes I and XIII). We sequenced microbial communities from samples representative of the lakes (sediments cores and water column) and of the surrounding environments (soils and river inlets). By sequencing the 16S rDNA and spo0A gene markers, we expect to demonstrate that, among the total microbial community, endospores preserved in sediment cores are more similar to the community in the water column, compared to communities found in samples external to the lake. This would confirm an autochthonous origin of this fraction of the microbial community and would show that endospores evolve in the water column and reflect environmental lake history. This is an essential requirement for further paleoecological studies using endospores as a proxy.

Poster presentation abstracts

Poster N°18

Identification and assessment of national green infrastructures in Switzerland

Erica Honeck, University of Geneva

Arthur Sanguet, University of Geneva, Conservatory and Botanical Garden of Geneva

The main objective of the thesis is to identify priority conservation areas to create national green infrastructures in Switzerland. Computer models will be used to determine species distribution, corridors and landscape connectivity, as well as the flow of ecosystem services. Socio-economic data will be included in our analysis to optimize biodiversity conservation while minimizing implementation costs.

Poster presentation abstracts

Poster N°19

Amphibian decline in protected areas

Benedikt Schmidt, Info Fauna Karch & UZH

The loss of biodiversity is a defining feature of the Anthropocene. Nature reserves and other types of protected areas are commonly used to slow the decline of biodiversity and to preserve biodiversity within the reserves. Here we used data from a national monitoring program to assess how well nature reserves work. We focus on amphibians, a globally threatened taxonomic group, for which Switzerland established a system of nature reserves of national importance. The results show that amphibians decline in the reserves despite a high protection status. Species went extinct locally and abundances of the persisting species declined. We conclude that a better management of the nature reserves is necessary.

Poster presentation abstracts

Poster N°20

Identification and assessment of green infrastructures in Switzerland

Arthur Sanguet, Université de Geneve

Erica Honeck, Université de Geneve

The main objective of the thesis is to identify priority conservation areas to create national green infrastructures in Switzerland. Computer models will be used to determine species distribution, landscape connectivity and corridors, as well as the flow of ecosystem services. Socio-economic data will be included in our analysis to optimize biodiversity conservation while minimizing implementation costs.

Poster presentation abstracts

Poster N°21

Snow leopard site use in the Mongolian Altai-Sayan Ecoregion: the effects of preys and sympatric large carnivores

Claudio Augugliaro, University of Lausanne

Fridolin Zimmermann, KORA

Philippe Christe, University of Lausanne

Conservation strategies at landscape scales are needed to ensure the long-term persistence of the threatened snow leopards (*Panthera uncia*), its main preys, and sympatric large carnivores.

However, little is known about the snow leopard status in the Mongolian Altai-Sayan ecoregion, an area connecting the southern populations distributed in the Tibetan Plateau and the northern populations distributed in the Russian Altai-Sayan Ecoregion.

During autumn 2017 we conducted interview-based site-occupancy large scale surveys in Bayan Olgii province (Mongolia). The surveys included questions about snow leopards and co-occurring main preys and predators. We conducted a total of 285 independent interviews from local communities in 81 grid cells (15x15-km).

We aim to assess the influence of the presence of a key prey species, the Siberian ibex (*Capra sibirica*), the presence of sympatric carnivores like the wolverine (*Gulo gulo*) and the grey wolf (*Canis lupus*), and topographic features on probability of snow leopard occurrence across the province. We will estimate the detection probability on the basis of the respondent's knowledge and experience.

The results of these surveys should allow identifying priority areas for further field surveys (e.g. by means of camera traps) and reveals critical areas for the conservation of snow leopard in the province.

Poster presentation abstracts

Poster N°22

Reconstruction of genetic diversity from ancient DNA prior to recolonization of nearly extinct Alpine ibex (*Capra ibex*)

Mathieu Robin, University of Zurich
Christine Grossen, University of Zurich
Giada Ferrari, University of Zurich
Lukas F. Keller University of Zurich

The Alpine ibex (*Capra ibex*) was hunted extensively since the 16th century before near extinction due to a strong bottleneck in the 19th century. Only a small population survived in the Gran Paradiso National Park in

Italy. Reintroductions led to a recovery of the species but recent populations show very low levels of genetic variability. Although human influence seems the most parsimonious explanation for the low genetic diversity, genetic analysis in other species revealed a genetic depletion even before human induced bottlenecks occurred. Climatic changes during the Pleistocene or subsequent responses to Holocene changes in habitat distribution were considered as cause. Using an ancient DNA approach, we investigated how the mitochondrial genetic diversity of the Alpine ibex changed over time to tackle the cause of the depletion in genetic variability.

We were able to reconstruct Alpine ibex mitogenomes from six ancient samples (3300 BP to 8600 BP) and five historic samples (75 BP to 251 BP). We found a substantial reduction of Swiss haplotype diversity as only one out of eight recovered haplotypes were observed among recent populations. Moreover, we discovered different mitochondrial nucleotide diversities between ancient specimens in contrast to historic and recent Alpine ibex individuals. This indicates that the low genetic diversity in recent Alpine ibex populations is rather due to human influence during the last centuries than environmental changes in the past.

Poster presentation abstracts

Poster N°23

Spatial modelling of insect pests under climate change

Marc Grünig, Agroscope, ETH Zürich

Dominique Mazzi, Agroscope

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Loïc Pellissier, ETH Zürich

The changing climate is forcing species to adapt their ranges in order to follow preferred climatic conditions. Therefore, pressure from pests on crop plants will increase with climate change, thus requiring adaptation of crop protection measures. The development of these measures is supported by quantitative information on the future proliferation and spread of pests and pathogenic agents.

We use high resolution climate data and contemporary spatial distribution modelling approaches to prepare scenarios of the spread of certain harmful organisms relevant to the Swiss agricultural sector. With the results of the study we aim to inform on the risk of occurrence of new invasive insect pest species that are expected to invade Switzerland under future climate change and to evaluate the circumstances under which they could threaten the Swiss agriculture.

Poster presentation abstracts

Poster N°24

Plant-microbial interactions in organic and conventional farming systems: changes in responses to drought.

Emily Oliveira Hagen, Grassland Sciences, ETH Zürich, Agroscope Reckenholz

Yujie Liu, Grassland Sciences, ETH Zürich

Qing Sun, Grassland Sciences, ETH Zürich

Valentin Klaus, Grassland Sciences, ETH Zürich

Thomas Keller, Agroscope Reckenholz, Swedish University of Agricultural Sciences

Raphaël Wittwer, Agroscope Reckenholz, University of Zürich

Klaus Schläppi, Agroscope Reckenholz, University of Bern

Marcel van der Heijden, Agroscope Reckenholz, University of Zürich, Utrecht University

Nina Buchmann, Grassland Sciences, ETH Zürich

Models project a mean reduction in Swiss summer precipitation by mid of the century of around 15%. It is unclear, however, how different farming systems will cope with irregular and harsh climatic conditions and which is most resilient against climate change. Our goal is to compare four main Swiss arable farming systems (i.e. organic arable farming with tillage and reduced tillage and conventional arable farming with and without tillage) and test their response to simulated summer drought. For this, a severe drought will be promoted by rain shelters in maize, pea/barley and winter wheat fields. We will make use of the DNA metabarcoding method to assess the composition of the soil communities, targeting prokaryotes and eukaryotes. For prokaryotes, the ITS region will be targeted using a primer pair for the V5-V7 region of the 16S rRNA gene. For eukaryotes, we will use a method that simultaneously characterizes multiple eukaryotic organisms at species-level resolution in a single PCR reaction using multiple primers that target the ITS2 region. Finally, a socio-economic assessment will make use of all data collected and evaluate the economic consequences of drought for the four farming systems. Our results will contribute to i) a better understanding of important processes taking place at different farming systems, and ii) formulating proactive responses to climate change, allowing for gradual and informed adaptation to better meet agricultural goals.

Poster presentation abstracts

Poster N°25

Temperature regulates deterministic processes and the succession of microbial interactions in anaerobic digestion process

Qiang Lin, Institute of Soil Biology, Czech Academy of Sciences

Temperature plays crucial roles in microbial interactions that affect the stability and performance of anaerobic digestion. In this study, the microbial interactions and their succession in the anaerobic digestion process were investigated at three levels, represented by (1) present and (2) active microorganisms, and (3) gene expressions under a temperature gradient from 25 to 55 C. Network topological features indicated a global variation in microbial interactions at different temperatures. The variations of microbial interactions in terms of network modularity and deterministic processes based on topological features, corresponded well with the variations of methane productions, but not with temperatures. A common successional pattern of microbial interactions was observed at different temperatures, which showed that both deterministic processes and network modularity increased over time during the digestion process. It was concluded that the increase in temperature-mediated network modularity and deterministic processes on shaping the microbial interactions improved the stability and efficiency of anaerobic digestion process.

Poster presentation abstracts

Poster N°26

HEALTHIER OR BIGGER? Temperature-dependent melanism and phenoloxidase activity in the dimorphic fly *Sepsis thoracica*

Natalia Gourgoulianni, University of Zurich

Wolf U. Blanckenhorn, University of Zurich

Juan P. Busso, University of Zurich

Martin A. Schäfer, University of Zurich

Climate change alters both average temperatures as well as the frequency and severity of heat waves. Whereas numerous studies have investigated the effects of temperature on morphological and life history traits, current knowledge about temperature effects on immune function is still limited. We experimentally studied in the dimorphic dung fly *Sepsis thoracica* (Diptera: Sepsidae) how developmental temperature and larval density influences phenoloxidase (PO) activity, a key enzyme in insect pigmentation, thermoregulation and immunity, at the later adult stage. We raised flies from five latitudinal populations at three developmental temperatures (18, 24, 30). Overall our results indicate that morph- and sex-specific PO activity, and likely immune function, in *S. thoracica* depends on temperature and larval density, modifying the existing trade-off relationship between immunity and body size. The strong dampening of the immune system of all morphs at cool temperatures suggests low-temperature stress in this warm-adapted species. Lastly, our results support the population density dependent prophylaxis hypothesis, which predicts higher investment in immunity due to limited resource availability and increased pathogen infection probability.

Poster presentation abstracts

Poster N°27

Spatial predictions of essential biodiversity variables: a bird perspective

Amini Tehrani Nasrin, University of Lausanne

Jérôme Guélat, Swiss Ornithological Institute

Thomas Sattler, Swiss Ornithological Institute

Antoine Guisan, University of Lausanne

Poster presentation abstracts

Poster N°28

Influence of insect herbivores on alpine plant communities under climate change

Patrice Descombes, WSL

This poster will present the results of a 3 year experiment in the alps.

Poster presentation abstracts

Poster N°29

Change in invertebrate taxonomic and functional community composition along an urbanization gradient

Andrea Zanetta, University of Fribourg

Swiss Federal Research Institute WSL Birmensdorf

David Frey, ETH Zurich

Sven Bacher, University of Fribourg

Martin M. Gossner, Swiss Federal Research Institute WSL Birmensdorf

Marco Moretti, Swiss Federal Research Institute WSL Birmensdorf

Urban areas host a considerable degree of biodiversity, but it is still unclear how species assemblages react to increasing urban densification. To investigate the patterns underlying the variation of community composition among sites (β -diversity) we partitioned β -diversity into turnover and nestedness components. We applied this to taxonomic and functional diversity metrics, reflecting respectively replacement and reduction of species and functional trait space. We investigated whether patterns of β -diversity vary along the urbanization gradient. We hypothesize that the most important changes in β -diversity occur in the most densely urbanized areas, where landscape-fragmentation, habitat loss and filtering effects are expected to be strongest.

An extensive multi-taxa invertebrate survey was carried out in 85 gardens in the city of Zurich, resulting in a dataset of more than 1200 species. While taxonomic β -diversity of 8 selected invertebrate groups was predominantly characterized by turnover, functional β -diversity was mainly driven by nestedness and only partially by turnover. The urbanization gradient was an important driver of taxonomic and functional β -diversity of most invertebrate groups. Invertebrate species community composition changed along the entire urbanization gradient, while functional trait space variation was mainly linked to high levels of urban densification. Our results suggest a diverse urban invertebrate composition rather than biotic homogenization.

Poster presentation abstracts

Poster N°30

Do patch size distribution and patch connectivity in dendritic networks affect invasion success of species?

Kathrin Holenstein, University of Zurich / Eawag (Aquatic Research)

Eric Harvey, Eawag (Aquatic Research)

Emanuel A. Fronhofer, Eawag (Aquatic Research)

Florian Altermatt, Eawag (Aquatic Research)

Biological invasions, such as commonly observed in dendritic riverine networks, have a huge impact on changes in biodiversity or even loss of species and consequently threaten ecosystem functioning. Understanding invasion dynamics in complex networks thus becomes increasingly important. As habitat size, connectivity and dispersal properties are known to shape community dynamics, we hypothesized that they also affect the success of invading species. Using protist microcosm experiments we disentangled how patch size and patch connectivity affect the establishment success of invading species. We showed that a larger patch size as well as a high biodiversity in a patch immediately preceding an invasion reduced invasion success. Contrarily, connectivity did not have a direct effect on invasion success but indirectly affected invasions by shaping diversity patterns in the whole network.

Poster presentation abstracts

Poster N°31

Spatial and temporal dynamics of the Alpine Rock Ptarmigan (*Lagopus muta helvetica*) in Switzerland

Fabian Fopp, ETH Zürich

Loïc Pellissier, ETH Zürich

Harald Bugmann, ETH Zürich

Fränzi Korner, Vogelwarte Sempach

Lukas Jenni, Vogelwarte Sempach

The Alpine Rock Ptarmigan (*Lagopus muta helvetica*) is an Arctic grouse species which occurs above the tree line in the Alps. A significant decline of the population count has been observed over the last decades in Switzerland. Although several studies regarding this decline have been conducted in different regions of the Alps, it is still not completely clear what factors are causing this decrease in population count. Climate change however seems to lead to a reduction of suitable habitat.

Using different datasets of Ptarmigan recordings, I will build spatial models to investigate which environmental factors could have influenced the observed changes in their distribution, population count and reproductive success. The analysis includes climate data, changes in vegetation and alpine tourism as predictors.

The insights of my master thesis will hopefully lead to a better understanding of the temporal and spatial dynamics of the Rock Ptarmigan and help for future conservation measurements.

Poster presentation abstracts

Poster N°32

Demographic Buffering and Demographic Lability in Animal Populations

Omar Lenzi, University of Zürich

Dr. Maria Paniw, University of Zürich

Prof. Dr. Arpat Ozgul, University of Zürich

Dr. Rob Salguero-Gómez, Oxford University, MPIDR, University of Queensland

Temporal variation in vital rates like survival or fecundity can significantly decrease the fitness of a population. Therefore, species are expected to be buffered against this variation, showing a negative correlation between the variance of their vital rates and their contribution to fitness. However, some species profit from temporal variation in key environmental drivers. For such labile species, critical vital rates vary freely to track the environment change. Buffering and Lability have been linked to life-history strategies in plants, but their distribution in animals is unknown. Using demographic data from 30 animal populations in the COMADRE online database, we calculated buffering and lability for each population. We also projected each population through time and compared the stochastic population growth rate, λ_s , with deterministic λ_d to gain a more mechanistic understanding of buffering and lability. We expected the ratio λ_s/λ_d to be bigger in labile species. Our results show that, the ratio of λ_s/λ_d were not correlated with the correlation coefficients, indicating disagreement between phenomenological and mechanistic approaches. A possible reason for the lack of clear patterns in buffering vs. lability could be that animals show a narrower range of life-histories compared to plants. In the present context of climate change, we expect higher variability in the environment, and predicting the response of species can be critical in their management or conservation.

Poster presentation abstracts

Poster N°33

How to document plant-insect interaction networks?

Pitteloud Camille, ETHZ

Loïc Pellissier, ETHZ

The Lif3web project aims at unravelling the mechanisms that structure the interactions between plant and herbivores to forecast the impact of climate change on natural communities. Due to good dispersal abilities, herbivores are expected to track climate change faster than plants, shaping new co-occurrences and possibly interaction networks. This increase of herbivory pressure on alpine plant communities is expected to impact alpine plant communities, known to be poorly defended. The deep understanding of those processes first requires to document the current plant-insect interaction networks. In that context, DNA metabarcoding technique, when applied on insect faeces, is a highly informative tool to establish interaction networks. This NGS technique, here based on the amplification of nuclear and chloroplastic plant DNA markers, allows a rapid and accurate identification of the plant species that compose insect diets. This approach will be used to inform about grasshopper-plant interaction networks along eight elevation transects distributed across the Swiss Alps. The resulting ecological knowledge coupled with functional traits analyses is further used to unravel the mechanisms that are shaping those networks variations along the elevation gradient and to forecast the consequences of climate change on the structure and composition of alpine plant communities.

Poster presentation abstracts

Poster N°34

Disruption of pollination as a function of light intensity and distance from street lamps

Simone Giavi, University of Bern

Eva Knop, University of Bern

In the last century the artificial light at night (ALAN) has dramatically spread around the world but its consequences are still poorly studied. ALAN has been shown to alter various processes, such as the circadian rhythm of various plant and animal species or animal navigation. On a community level, it has recently been shown that ALAN can reduce the activity of entire nocturnal flower visitor communities, with negative consequences for the pollination service they provide. However, we currently do not know up to which light intensities flower visitations are affected and/or whether the effect is dependent on the distance from the light source. We assessed the frequency of flower visitations in relation to light intensity and distance on a total of 16 ruderal meadows in the Bernese pre-alps. Eight of the sites were experimentally illuminated with an LED street lamp, the other eight were kept in the dark as controls. In addition, we investigated the impact of light intensity and distance from the light source on the seed output of several plant model, one of which (*Silene latifolia*) is mostly pollinated during night by various moth species among which is *Hadena bicruris* whose larvae is a seed predator. We expect lower number of flower visitors and reduced seed set with light intensity and proximity to the lamp. Due to the attraction of the lamp from far distances, we further expect a negative effect also when light intensities are similar to natural dark conditions.

Poster presentation abstracts

Poster N°35

Inference of microbial interaction networks from large-scale data sets through causal knowledge discovery

Janko Tackmann, University of Zürich

João F. Matias Rodrigues, University of Zürich

Christian von Mering, University of Zürich

The recent explosion of metagenomic sequencing data makes tools for rapid computational analysis essential. While scalable software for mapping and clustering of Operational Taxonomic Units (OTUs) is available, prediction of microbial interactions based on co-occurrence is still lagging behind. Furthermore, most current tools for ecological network inference suffer from high numbers of false positives, since they typically i) do not distinguish between direct and indirect interactions and ii) do not consider environmental and technical variables. These factors can induce widespread association signals in composite datasets with samples from diverse habitats, conditions and experimental protocols.

We present FlashWeave, a software tool which adopts an approach from the causal inference field to infer highly resolved microbial interactions from large data sets. FlashWeave seamlessly integrates environmental and technical variables, with optional adjustment for latent confounding factors.

The method is highly optimised for speed, scaling to tens of thousands of OTUs and samples, surpassing state of the art methods on average by two orders of magnitude. In benchmarks on a variety of synthetic data sets, it provides accuracy comparable to or surpassing current methods. We apply FlashWeave to a large-scale meta-dataset of 69,818 public human gut samples to infer one of the largest and most diverse networks of microbial interactions in the human gastrointestinal tract to date.

Poster presentation abstracts

Poster N°36

Demographic responses of resurrected rotifers to changing environmental conditions

Federica (Romina) Schanz, University of Zurich, DEBES, Population Ecology

Stefan Sommer, University of Zurich, DEBES, Population Ecology

Dr. Diego Fontaneto, National Research Council, Institute of Ecosystem Study

Prof. Dr. Arpat Ozgul, University of Zurich, DEBES, Population Ecology

Adaptation allows populations to persist in changing environments. These adaptations manifest themselves as changes in life-history responses. We investigated whether *Brachionus calyciflorus* adapted to changing copper concentrations in the polluted Lake Orta (Italy) and tested for a food density effect. Thereby, we resurrected resting eggs from sediment layers of 3 pollution periods. We recorded life-table data of 504 rotifers, which we kept individually at 3 copper concentrations and 2 food densities. With the data, we estimated vital rates and resulting population growth rates λ . We then run perturbation analyses to assess vital rate contributions to λ differences among treatments and to investigate how future vital rate changes would affect λ . We found a negative copper effect on vital rates and λ , but no adaptation to copper pollution because of similar demographic responses between the periods. Food density had no positive effect on copper tolerance. Moreover, adult survival, the probability of being an amictic adult (i.e., producing female offspring) and amictic adult's fecundity contributed most to observed λ differences, whereas λ were most elastic to juvenile and adult survival. Overall, the results revealed that adult survival is the key mechanism of rotifer responses to copper pollution. However, we did not find signs of adaptation. Resurrection ecology provided mechanistic insights into life-history responses to environmental pollution of a common species.

Poster presentation abstracts

Poster N°37

Barn owl (*Tyto alba*) foraging strategies and habitat selection

Robin Séchaud, Department of Ecology and Evolution, University of Lausanne

Kim Schalcher, Department of Ecology and Evolution, University of Lausanne

Alexandre Roulin, Department of Ecology and Evolution, University of Lausanne

Agriculture is the most represented land use across Europe and many species rely directly on this ecosystem. However, its recent intensification and modernization has transformed the landscape and led to a dramatic loss of farmland biodiversity. The barn owl (*Tyto alba*) is a typical example of a farmland synanthropic species whose population suffered a decline in Europe over the past decades due to the homogenisation of the environment. For effective conservation and population management one requires knowing which habitat categories comprise a barn owl's suitable home range and its preferred foraging grounds. In this study, we monitored 78 barn owl broods from hatching to fledging and equipped the parents with GPS tags, in parallel with high resolution habitat mapping. We estimated home range composition and assessed foraging habitat selection. The analyses showed a strong preference for extensively exploited areas such as wild flowers, grasslands and pastures. Higher proportions of such preferred habitats within a home range was associated with higher fledgling fitness. Additionally, male and female parents differ in prey provisioning, time budget and hunting techniques. In conclusion, our study highlights the importance of extensively exploited habitats for breeding barn owls and strong differences in hunting effort and time allocation between sexes.

Poster presentation abstracts

Poster N°39

Variations in Body Condition in Humpback whales

Charlotte Bellot, University of Neuchatel

Humpback whales (*Megaptera novaeangliae*) are well known to migrate between breeding grounds and feeding areas and could travel as far as 16.000 miles which make them one of the furthest migrating species in the world. However, little is known on the pattern of migration and the conditions whales go through during the travel. Girth of the body is directly correlated to fat content and so, body condition of the individual. And because they completely forgo eating during mating months living on their fat stores, body condition is correlated to their health state.

Our analyses used a drone which flying above the individuals and filming them during the surfacings. Images are then analysed with R software allowing photogrammetry and allometry measurements.

The aim of the study is to estimate the inter seasonal variations in body condition and to highlight body sections varying the most depending on different variables such as: status of the whale, age, gender...

Another part of the study will try to find evidence of correlations between the size of some parts of the whale (such as the mouth) and body condition.

We assume that during breeding season, individuals (especially pregnant females) are bigger than the ones during feeding season.

Long term goals of this study are to validate a new non-invasive method to estimate body condition in free-ranging marine mammals and to better understand whales' needs to be able implementing conservation measures in their feeding areas.

Poster presentation abstracts

Poster N°40

Malaria infection in mosquitoes decreases the personal protection offered by permethrin-treated bed nets

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Insecticide-treated bed nets (ITNs) are currently the most cost-effective way of controlling malaria. They protect individuals by repelling mosquitoes, and thus reduce the risk that users are bitten by infectious mosquitoes; they protect the community by killing mosquitoes before they become infectious. To fully understand and predict how ITNs affect the epidemiology of malaria, we must know how malaria affects both types of protection. Since malaria infection makes mosquitoes more motivated and persistent when attempting to blood feed, we expected it would also influence the extent to which mosquitoes are repelled. Indeed, in a lab and a field experiment, we found that mosquitoes harbouring the infectious stage of malaria were less repelled by a permethrin-treated net than uninfected ones. Thus, malaria reduces the personal protection offered by ITNs at the stage where it is most needed. Further studies must show whether the lower personal protection is balanced by greater community protection.

Poster presentation abstracts

Poster N°41

The impact of global change on the abundance and impact of grassland pathogenic fungi: results from the PaNDiv experiment

Seraina Cappelli, Uni Bern

Noémie Pichon, Uni Bern

Eric Allan, Uni Bern

Foliar fungal pathogens are abundant in grasslands where they can affect productivity. Their prevalence may be impacted by changes in plant diversity, functional composition and nitrogen. Nitrogen enrichment is a global change driver and may affect pathogens directly or indirectly via changes in community composition. The relative importance of these different pathways in determining pathogen prevalence and impact is unknown. The PaNDiv experiment crosses foliar fungal pathogen exclusion with nitrogen fertilization, plant diversity and functional composition treatments. The exclusion of pathogens increases aboveground biomass production, demonstrating that foliar fungi can affect grassland ecosystem functioning. We observed that plants with a conservative, slow growing strategy had lower infection than fast growing species, which provides evidence for a growth-defence trade-off. Fungal infection increased with host density, providing evidence for resource concentration effects. The strength of the host concentration effect depended on plant diversity and was strongest in diverse plant communities, perhaps indicating that plant diversity increases the susceptibility of hosts to pathogens. This shows that global change can affect pathogen abundance through multiple mechanisms and imply that nitrogen fertilization will increase pathogen abundance primarily by reducing species diversity and shifting plant species composition towards a higher abundance of fast growing species.

Poster presentation abstracts

Poster N°42

The climatic niche and distribution limits in species of the Brassicaceae family in Switzerland

Theofania-Sotiria Patsiou, University of Basel

Nora Hohmann, University of Basel

Yvonne Willi, University of Basel

Climate is a strong driver of species distribution limits in plants, which suggests that there is some universal genetic constraint in the evolution of the climate niche that prevents range expansion. If so, one or a few aspects of the climate should determine niches and spatial distributions across species most strongly. We tested the hypothesis by screening 10 topo-climatic variables for their importance in explaining the distribution of 110 Brassicaceae species within Switzerland. We run species distribution models (SDMs) and calculated Huisman-Olf-Fresco (HOF) response curves for the most important climate variables. We found that minimum temperature of the coldest month (Bioclim 6) was the most important variable for the majority of species, followed by temperature seasonality (Bioclim 4) and mean temperature of the wettest quarter (Bioclim 8). HOF response curves indicated an asymmetric optimality curve for Bioclim 6 for most species. In conclusion, our results indicate that one aspect of the climate, minimum temperature during the cold period of the year, seems to prevail in explaining species' distributions in the Brassicaceae of Switzerland, supporting the hypothesis of universal constraints to niche evolution.

Poster presentation abstracts

Poster N°43

A historical legacy of antibiotic utilization on bacterial seed banks in sediments

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The introduction of antibiotics for both medical and non-medical purposes has had a positive effect in human welfare and agricultural output in the past century. However, there is also an important legacy in the use and disposal of antimicrobial agents in natural ecosystems. This historical legacy was investigated by quantifying two antibiotic resistance genes (ARG) conferring resistance to tetracycline (*tet(W)*) and sulfonamide (*sul1*) in bacterial seed bank DNA in sediments. The industrial introduction of antibiotics caused an abrupt increase in the total abundance of *tet(W)* and a steady increase in *sul1*. The abrupt change in *tet(W)* corresponded to an increase in relative abundance from ca. 1960 that peaked around 1976. This pattern of accumulation was highly correlated with the abundance of specific members of the seed bank community belonging to the Phylum Firmicutes. In contrast, the relative abundance of *sul1* increased after 1976. This correlated with a taxonomically broad spectrum of bacteria, reflecting *sul1* dissemination through horizontal gene transfer. The accumulation patterns of both ARGs correspond to the temporal scale of medical antibiotic use. Our results show that the bacterial seed bank can be used to look back at the historical usage of antibiotics and resistance prevalence.

Poster presentation abstracts

Poster N°44

Does habitat use influence social behaviour and cognitive performance in marine cleaning gobies?

Renata Mazzei, University of Neuchatel
Marta Soares, CIBIO, University of Porto
Redouan Bshary, University of Neuchâtel

There is evidence that variation in the complexity of both the ecological and social environment may influence the cognitive performance of individuals. The facultative cleaning goby species *Elacatinus prochilos* appears to provide an ideal system to study such environmental effects on individual cognitive performance. In this species, sponge-dwellers live in large groups and hardly clean other reef fishes, while individuals living openly on reef substrate live in small groups (often pairs) and obtain most of their food from cleaning interactions. We conducted two paired-choice experiments in which gobies had to identify and seek a food-providing plate either due to its pattern or due to its location in the aquarium. We predicted the former to be more ecologically relevant to cleaners (as client patterns may indicate their food value) and the latter to be more relevant for sponge-dwellers (finding food locations in a 3-dimensional space). Contrary to our expectations, both cleaners and sponge-dwellers largely failed in the cue task and performed similarly well in the spatial task. Additional laboratory observations indicate that gobies are very similar in both intraspecific social behavior and interspecific cleaning behavior, which might explain why they have similar performance in both tasks. Finally, *E. prochilos* have less frequent and less complex cleaning interactions with their clients, which might explain why the gobies performed poorly in the cue task.

Poster presentation abstracts

Poster N°45

Evaluating the effect of ectoparasites on host fish metabolism using an individual-level approach

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Dominique Roche, University of Neuchâtel
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Ectoparasites can impose substantial physiological costs to their hosts including tissue damage, blood loss, and activation of an immune response. As a result, ectoparasites may alter the energetic requirements of their hosts. Although some studies have shown that ectoparasite infection leads to increased host standard metabolic rates (SMR), a proxy for basal energy expenditure, few have evaluated whether SMR measures are repeatable in healthy individuals, nor how an individual's SMR changes following parasite exposure. We used resting respirometers to measure SMR and maximum metabolic rate (MMR) twice each in 64 uninfected Ambon damselfish (*Pomacentrus amboinensis*) and estimated the repeatability of these traits in wild-caught fish. We then exposed half ($n = 32$) of the fish to an experimental culture of blood-feeding gnathiid isopod ectoparasites, while the remaining fish were similarly manipulated, but remained uninfected. We re-measured MMR and SMR in all fish following 17 days of parasite or control treatments to test whether infection led to changes in the metabolic rates of infected hosts. Our preliminary results suggest that infection with gnathiids results in increased SMR and MMR in fish hosts exposed to our experimental culture. These results, combined with information on how infection affects individual-level behavioural traits, will help increase our understanding of the costs imposed by parasites on wild animal hosts.

Poster presentation abstracts

Poster N°46

How do female *Diabrotica* beetles defend their eggs?

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Several herbivore insects are able to hijack defensive secondary metabolites from their host plant and use them against their natural enemies. While these effects are well documented for insect larvae and adults, it is still poorly understood whether sequestered metabolites can be transferred to eggs as a defensive mechanism. In this study, we profiled the chemical composition of the eggs of the benzoxazinoids (BXD)-sequestering *Diabrotica virgifera* and of the non-BXD-sequestering *D. balteata*, and evaluated egg preference for *Atheta coriaria*, a tiny predatory beetle. In choice and no-choice experiments, *A. coriaria* ate 2 to 3-times more *D. balteata* eggs than *D. virgifera* eggs. To gain mechanistic insights into the potential chemical mechanism that may mediate the observed preference, we measured egg primary and secondary metabolites, as well as egg volatile organic compounds (VOCs). We found that *D. balteata* eggs are of lower nutritional quality, emit higher amounts of potentially attractant volatiles and contain lower concentrations of toxic benzoxazinoids compared to the eggs of *D. virgifera*. We are currently conducting behavioral and manipulative experiments to determine the relative contribution of these differences in the chemical composition of the eggs to the observed predator preference. Our study will help to understand the factors that determine the differential predation of *D. virgifera* and *D. balteata* eggs.

Poster presentation abstracts

Poster N°47

Targeted mycophagous lifestyle of *Lysinibacillus sphaericus* against the phytopathogenic fungus *Rhizoctonia solani*

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Bacteria are well known for their diversified nutritional capabilities, which may lead to positive or negative interactions with other organisms. Mycophagy is a behavior allowing bacteria to obtain nutrients from living fungi, with a negative impact on the fungal partner. Bacilli are an important component of the soil microbial community and are widely used in biofertilization and biocontrol. We observed a mycophagous lifestyle in *Lysinibacillus sphaericus* against phytopathogenic fungus *Rhizoctonia solani*. In order to understand this mechanisms, a confrontation assay was performed, where *R. solani* biomass and its exudates were the sole carbon source. In order to assess the specificity of the interaction, we also confronted *L. sphaericus* to a saprophytic fungus, *Trichoderma reesei*. *L. sphaericus* inhibited the growth of *R. solani* but not of *T. reesei* and was able to disperse on the fungal hyphae of both fungal species. Only *R. solani* hyphae that were in direct contact with bacteria were adversely damaged and unable to re-grow. Microscopic observations revealed the deformation of *R. solani*'s cell wall and bacteria penetrating fungal hyphae. Bacterial growth occurred at the expense of *R. solani* fungal mycelium only. This confirms that the living mycelium of *R. solani* is required for bacterial growth and the ability of the bacterium to select its target. This yet unexplored mycophagous lifestyle could be exploited for the control of phytopathogens in sustainable agriculture.

Poster presentation abstracts

Poster N°48

Response of biodiversity to urbanization and urban green infrastructure across Europe. Design and hypotheses

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Urbanization is one of the main drivers altering biodiversity from the individual to the ecosystem level. It reduces, fragments and deteriorates the amount of available habitat. Furthermore, it introduces new disturbances (e.g. pollution) and disrupts species interactions, such as competition or parasitism, by introducing exotic species or promoting few native ones (e.g. honeybees). Nonetheless, urbanization is not a uniform process. There is compelling evidence that certain urban designs can support native biodiversity that provide ecosystem services and functions. Particularly, the spatial configuration and composition of green infrastructure and the degree of urban compaction are key factors influencing the connectivity, quality, quantity and heterogeneity of urban habitats ultimately determining the ecological and conservation value of cities. The goal of this project is to study the influence of urbanization and urban green infrastructure on biodiversity from a local (Zürich) to a European scale (including Antwerp, Paris, Poznan, Tartu and Zürich) and following a multi-taxa (bees, wasps, bats and nocturnal insects) approach. Analytically, we will use a combination of data ranging from individual traits, demography, interaction networks and taxonomic and functional community composition. The results of this study should lead to a better understanding of the ecology of urban environments applicable to improve city design and planning in an urbanizing world.

Poster presentation abstracts

Poster N°49

Which are the worst aliens?

Lara Volery, University of Fribourg

Divija Jatavallabhula, University of Fribourg

Sven Bacher, University of Fribourg

Alien species can cause serious damage to the environment and socio-economy, but most alien species are harmless. More than 14000 alien species are known from Europe alone and we cannot manage them all. In order to efficiently use the limited resources for conservation, we need to identify the most harmful invaders. Two methods have been recently developed: one to compare all kinds of environmental impacts across all taxa (the Environmental Impact Classification of Alien Taxa - EICAT), and one to compare all kinds of socio-economic impacts across all taxa (the Socio-Economic Impact Classification of Alien Taxa - SEICAT). These methods are analogous to the widely known Red List of Threatened species and EICAT has recently been adopted by the IUCN. Such comparisons of impacts will allow us to prioritize species causing high impacts for management (Black Lists), to identify traits of alien species with high impacts as well as regions or habitats under risk, and to forecast future invasive species. However, impact assessments are still subject to uncertainty which might lead to inconsistencies in prioritization of alien species. We are currently developing concepts to identify and incorporate uncertainty into S/EICAT assessments.

Poster presentation abstracts

Poster N°50

Rapid Adaption in Experimental Grasslands

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Several biodiversity experiments, including the long-term Jena Biodiversity Experiment, have shown effects of experimental species diversity on measures of plant, community and ecosystem performance. However the question remains, whether these effects are a result of plant's phenotypic plastic response to differing microclimate in communities, or due to genetic selection of better adapted progeny. We used a common garden approach with seeds of the 10-year-old plant communities of the Jena Experiment. We grew progeny of 18 plant species, including grasses, herbs and legumes, which originates from communities representing an experimental diversity gradient from monocultures to 60-species mixtures. We grew each individual in a separate pot for two years. Then we measured multiple above-ground plant traits related to vegetative and generative growth. We found plant traits in the common garden unrelated to the species diversity of the experimental communities in the Jena Experiment. We conclude that the progeny remains very plastic in its phenotype, possibly mitigating selection pressure. Additional implications for generalization, soil-plant feedback, and influence of light availability are discussed.

Poster presentation abstracts

Poster N°51

The consequence of plant domestication for resistance against insects: testing the role of the plant-breeding target

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Plant domestication has generally resulted in decreased chemical and physical defense in crop plants compared to their wild ancestors. A reduction in plant defensive traits is often expected to result in increased insect performance. However recent studies have shown that this pattern is not ubiquitous.

The reason for this may lie in the purpose or the organ targeted by domestication. Such that, a positive relationship between reduction in plant defense and increased insect performance will be only, or more evident for cultivars and plant organs that have been selected for consumption.

To test this hypothesis we used cultivated varieties of squash (genus Cucurbita) and larvae of one herbivore: *Diabrotica balteata* (root-feeding herbivore) which co-evolved with Cucurbitaceae.

We chose cultivated varieties that have been selected for different purposes (fruit consumption and ornamentals). Plants were analyzed for their concentration of cucurbitacins in roots that are known to be toxic to generalist herbivores.

We found support for our hypothesis; cucurbits domesticated for fruit consumption have a reduction of toxic compound. *D. balteata* larvae prefer squash root containing cucurbitacins.

These results highlight the importance of incorporating plant traits and insect adaptations in studies on crop domestication and insect interactions.

Poster presentation abstracts

Poster N°52

Exploring the phylogeography of hyalospheniid testate amoebae (Amoebozoa) from regional to sub-continental scales.

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Molecular techniques are revealing a considerable cryptic diversity in many protist groups. These organisms have been traditionally pooled together within single species, leading to wrong conclusions on their ecology and geographical distributions. Testate amoebae are a group of ecologically specialized protists which represent a good model to test ecological, biogeographical and phylogeographical hypotheses. Previous studies showed that the diversity of genus *Nebela* was underestimated, even in well surveyed environments, and hosted a large diversity of species differing in their ecological optima. We surveyed the diversity of family Hyalospheniidae (Arcellinida, Amoebozoa) with focus on genera *Padaungiella*, *Alocodera* and *Apodera* (hereafter referred to as subfamily Apoderinae) and genus *Nebela*, based on COI barcoding and environmental DNA survey. We surveyed different geographical locations and/or environment types (Europe, Zealandia, North and South America). Most diversity of Apoderinae was found in Southern Hemisphere locations, suggesting a Gondwanaland origin for the group. A new form was found, diverging clearly in its COI sequence, which lead us to propose a new genus (*Paulistella*). Furthermore, morphometric and genetic data allowed us to split morphospecies of supposedly pan-gondwanian distribution into several units with geographically limited distributions. Finally, we discovered a novel diversity in genus *Nebela* that suggests phylogenetic niche conservatism.

Poster presentation abstracts

Poster N°53

Global Assessment of the environmental impact of alien ungulates

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Lara Volery, University of Fribourg

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Sven Bacher, University of Fribourg

Alien mammals have a high potential to cause negative impact in their introduced environment. Efforts are being put into place to quantify these impacts. A framework has been recently developed and adopted by the IUCN for comparing and classifying the environmental impacts of all alien species across taxa according to their magnitude (the Environmental Impact Classification of Alien Taxa - EICAT).

In our study, we classified the impacts of alien ungulates worldwide using this framework, based on all available published material reporting an impact of the alien on native species in its introduced environment. We identified species with the highest impacts, the most commonly documented mechanisms used by ungulates to cause damage and how these impacts varied across a geographic range. This information can not only help prioritise alien mammals for management purposes but also help fill gaps in the data that should be addressed in future research.

Poster presentation abstracts

Poster N°54

How do land-use intensification and biodiversity loss affect ecosystem resilience? A meta-analysis of manipulative experiments

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Santiago Soliveres, University of Bern

Eric Allan, University of Bern

Markus Fischer, University of Bern

Biodiversity is expected to increase ecosystem resilience while land-use intensification may reduce it either via a direct negative effect on ecosystem functioning or indirectly via a negative effect on biodiversity. To address this question, we synthesized available evidence from manipulative experiments performed across a land-use intensity gradient in 150 temperate agricultural grasslands, within the framework of the Biodiversity Exploratories. This allows for an analysis across trophic levels, types of function and types of disturbance. We quantified resilience using response ratios between treatment and control measures and fitted a mixed-model to control for temporal and spatial dependencies between variables and account for other covarying environmental factors such as soil fertility and topography. Our analysis showed no clear overall effect of biodiversity or land-use intensity on resilience. However, there was an interaction between the type of experimental treatment and biodiversity which showed a negative effect on resilience to fertilizer addition but had no effect on resilience to other disturbances, such as increased mowing intensity. Additionally, effects of biodiversity appear to be stronger for aboveground than belowground measures. These results indicate that effect of land-use or biodiversity on resilience depend on several factors like the type of disturbance or whether the ecosystem function is measured above- or belowground.

Poster presentation abstracts

Poster N°55

Biotic Factors Constraining Species Distribution

Dario Sanchez Castro, University of Basel

Poster presentation abstracts

Poster N°56

Emergent spatial patterns and biodiversity maintenance

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Teodora David, Laboratory of Microbiology, University of Neuchâtel

Annick Lambelet, Laboratory of Microbiology, University of Neuchâtel

Sevasti Filippidou, Laboratory of Microbiology, University of Neuchâtel

Martin Pion, Laboratory of Microbiology, University of Neuchâtel

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Redouan Bshary, Laboratory of Eco-ethology, University of Neuchâtel

Pilar Junier, Laboratory of Microbiology, University of Neuchâtel

In ecology, the competitive exclusion principle postulates that competition between two species with niche overlap and coexisting in the same environment eventually leads to the extinction of the less competitive species. However, previous experiments have shown coexistence at a local scale between two strains of the bacterial species *Pseudomonas putida* (wild-type GFP- and antibiotic-resistant UWC1 mCherry-labelled) growing in a homogeneous environment. Coexistence was linked to the emergence of self-organizing spiral-like spatial patterns. However, is coexistence stable over time? To answer this, sequential sub-culturing from the center and the edge of a colony, initially inoculated at a 1:1 ratio of the two *P. putida* strains, was performed after 24h of incubation on a minimal medium. Image analysis and flow cytometry were used in order to quantify the relative proportions of the two differentially-labeled strains in the entire colony. We observed coexistence is maintained in the center of the colony over time. However, there is exclusion of the less competitive *P. putida* UWC1 mCherry in the edge of the colony as it could be expected by the additional antibiotic-resistance gene present. Indeed, *P. putida* UWC1 mCherry has a lower division rate under non-selective conditions. As fungal networks are thought to be a strong structuring factor of bacterial communities in complex environments such as soils, additional experiments will now be conducted to address this issue.

Poster presentation abstracts

Poster N°57

Primitive plants: Plentiful but neglected resources for herbivores?

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Ted Turlings, University of Neuchâtel

Gregory Röder, University of Neuchâtel

Plants and their herbivores are engaged in a co-evolutionary arms race, whereby plants evolve strategies to cope with herbivores and the herbivores evolve traits to overcome these strategies. Some plants may also be avoided by herbivores because they lack suitable nutrients for development. Interestingly, primitive plants like mosses and ferns do not exhibit advanced defences, but are rarely eaten by herbivores. It has been hypothesised that their tissues are of poor nutrient quality, but this awaits scientific confirmation.

Here, the nutritive suitability of various mosses and ferns for two likely generalist herbivores was investigated using feeding assays combined with analytical quantification of nutrients. Growth and survival of a caterpillar (*Spodoptera littoralis*) and a snail (*Cochlicella barbara*) were assessed on fifteen species of mosses and ferns, and compared to their performance on maize plants, a well-studied angiosperm. In parallel, proteins, amino acids and sugars were measured in these plant species.

Overall, our results suggest that the poor performance of herbivores on primitive plants is not correlated with nutritional quality. Herbivore development and survival were considerably better on maize, whereas nutrient content varied strongly among plant species. Interestingly, taxonomically related species had similar levels of proteins, but not sugars. The results are discussed from an evolutionary perspective of plant defences against herbivory.

Poster presentation abstracts

Poster N°58

Cold hardiness of *Trichopria drosophilae*, a parasitoid of *Drosophila suzukii*

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Trichopria drosophilae (Hym: Diapriidae) is a hymenopteran parasitoid of *Drosophila* recorded from several parts of the world. It is currently considered for augmentative biological programs to control the invasive agricultural pest *Drosophila suzukii*. To evaluate its establishment potential in temperate regions, we characterized low temperature tolerance of a colony of *T. drosophilae* captured in 2017 from Zürich. To find the supercooling points (SCPs), unfed 2-day-old adults of *T. drosophilae* were cooled down at 1.0 °C min⁻¹. The results showed mean SCPs of -27.7 ± 0.95 for males and -27.1 ± 0.98 °C for females. In order to assess cold hardiness, unfed 2-day-old adults were exposed to constant low temperatures of +5, 0, -5, -10 and -17 °C. Prior and subsequent to the exposure, adults were acclimatized for 6 h at 12 °C for prohibiting cold stress. Survival as well as reproduction ability of females was recorded after cold exposure. At -17 ± 1 °C, 50% of individuals had died after 1 h exposure, while all were dead after 2 h. At -10 ± 1 °C few adults were alive after 6 h and all died within 24 h. At 0 °C and -5 °C, no adult survived 11 d of exposure. Cooled females at -17 ± 1 °C after 1 h exposure could produce offspring as well as females cooled at -5 °C for 8 d. Further researches will investigate how well different stages of this parasitoid can tolerate low temperatures to evaluate the potential of *T. drosophilae* as a biological control agent of *D. suzukii* in temperate regions.

Poster presentation abstracts

Poster N°59

Biocontrol potential of an encapsulated microbial consortium on the fungal pathogen *Rhizoctonia solani* in lettuce (*Lactuca sativa*)

Clément Etter, Laboratory of microbiology, University of Neuchatel

Plant pathogens are a threat for agriculture causing major yield losses. Pesticides used to protect crops pose serious environmental and health problems and resistance can occur. A sustainable alternative is microbial biocontrol. However, commercially available products usually contain single microbial species while it has been shown that many species interacting together is more efficient for pathogen control. It is also often difficult for the inoculated microbes to survive harsh conditions in soil. Thus, we investigate the effect of an immobilized microbial consortium in agar bead on the development of the soil-borne fungal pathogen *Rhizoctonia solani* using lettuce (*Lactuca sativa*) as host plant. The consortium consists of the fungus *Trichoderma reesei* and the bacteria *Lysinibacillus sphaericus* and takes advantage of the fungal highways concept for the delivery of bacteria. The use of a microfluidic device showed that bacteria are transported by the fungal mycelia and the consortium affects negatively *R. solani* by cell wall disintegration. Finally, a greenhouse and field experiment will reveal if the encapsulated consortium has a positive effect on lettuce health and growth by controlling *R. solani* infection. Put together, the data will consolidate the proof-of-concept that a consortium is more effective at controlling a plant pathogen than a single species-based biocontrol system and that the immobilization provides protection and augment root colonization capacity.

Poster presentation abstracts

Poster N°60

Oxalotrophy as a biocontrol strategy against phytopathogenic fungi

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The rise of the bio-market and the enhanced resistance of pathogens to conventional control methods have fostered the development of alternative control strategies for improving plant growth. Phytopathogenic fungi, such as *Botrytis cinerea* and *Rhizoctonia solani*, have a wide host range and cause economically important damage in crops worldwide. These pathogens use organic acids - and more precisely, oxalic acid - as a virulence factor. Degradation of this organic acid could be a new approach of biological control of fungal pathogens. Oxalotrophic bacteria are found in various environments, and use oxalate as carbon and energy source. Thus, they could provide a protection to the host against the pathogen, through nutritional interference. Confrontation experiments in Petri dishes with *B. cinerea* showed growth control in different culture media by *Cupriavidus necator* and *Cupriavidus oxalaticus*, two oxalotrophic soil bacteria. Control of *R. solani* is less pronounced with the same bacteria. In contrast, the non-oxalotrophic bacterium *Pseudomonas putida* exerts an intense pressure on *R. solani* on R2A medium. Further investigation needs to be done, in order to characterize the interaction between phytopathogenic fungi and oxalotrophic bacteria before doing in-vivo experiments in lettuce as a plant host.

Poster presentation abstracts

Poster N°61

Bacterial-fungal interactions and fungal highways : Probing mechanisms at the single cell level using microfluidics

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Bacterial-fungal interactions have an important position in soil functioning because both organisms take part in processes such as organic matter mineralization and mineral weathering. This close association can be illustrated through fungal highways (FH), described as the use of fungal hyphae by motile bacteria to move. The aim of this project is to give new insights on the mechanistics of FH using single cell level analysis. The oxalate-carbonate pathway (OCP) is used as a model system as FH have been demonstrated to be important for the functioning of this ecosystem process. By using microfluidics devices with two fungi, two bacteria and four growth media we test the effect of biotic interactions as well as trophic relations. We expect to observe variations of hyphal numbers and diameter, branching event as well as fungal cell wall thickness. We expect these to be related to the carbon source in the medium and the different associations of organisms. Preliminary results already showed significant differences for fungi grown in Malt-agar compared to Angle medium. Fungi growing in calcium oxalate as sole carbon source displayed less hyphae and thinner cell diameter in the microchannel. In additional experiments, efficiency of bacterial dispersal using fungal hyphae will be tested by adding bacteria and compare the effect of this on fungal morphology. Finally, we aim to obtain new insight on the OCP by focusing on fungal oxalotrophy and chemotactic movement of bacteria.

Poster presentation abstracts

Poster N°62

Endofungal bacteria - New insights into bacterial-fungal coexistence

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Bacteria and fungi coexist in various microhabitats, and their interactions directly impact higher trophic levels and thus nutrient cycling. Therefore, the study of bacterial-fungal interactions (BFI) and their importance on the functioning of different systems can raise and answer biological and ecological questions. Bacteria and fungi in close physical contact show relationships ranging from random coexistence to nearly total dependency. The conditions triggering changes in the type of interaction between both partners are key to understand the dynamics of BFI. The most intimate relationship described up to now consists in bacteria colonizing inner hyphae (endobacteria). In this study, we have investigated the diversity of endobacteria, or bacteria firmly attached to hyphae, in our fungal strain collection. In addition to this, we have tried to understand basic rules underpinning this close association. We have discovered that endobacteria are much more frequent than previously assumed. Moreover, they seem to appear equally distributed in the phyla Basidiomycota, Ascomycota and Zygomycota and also occur in the distinct phylogenetic lineage of the eukaryotic fungus-like Oomycota. Furthermore, we highlighted that under certain stress conditions for the fungal host, this tight relation turns to a loose coexistence of both partners.

Poster presentation abstracts

Poster N°63

Microbial diversity and ecosystem functioning and services in vineyards

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Anne-Laure Fragnière, University of Fribourg

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The PromESSinG project (www.promessing.eu, financed by BiodivERsA/FACCE-JPI) investigates the links between soil management, soil biodiversity and ecosystem functions in vineyard ecosystems in five European countries (CH, F, D, A, ROM). In standardized experiments replicated in each country, we investigate how different levels of vegetation removal in vineyards affect soil microbial community structure and function. In particular, we study effects on soil respiration and decomposition rates as well as on diversity and community structure of soil protists, fungi and bacteria. Furthermore we evaluate the effects of soil management on different indicators of grape quality by FTIR spectroscopy. Here, we present first results obtained in Switzerland. In preliminary analyses we found that vegetation removal had only weak effects on diversity or community composition of microorganisms, but selectively affected soil functions and grape quality parameters. These results indicate that vegetation in vineyards has an overall positive effect on soil health and potentially requires compensation measures by the winemaker in order to avoid compromising grape quality.

Poster presentation abstracts

Poster N°64

Vocal communication involved in Nesting Behaviour of Wild Chimpanzees

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Nesting behaviour, which is building sleeping nests in trees by folding branches or leaves, is shared by all great apes species. In chimpanzees, the evolution of this behaviour, the function of nests, the way they are built and their composition have been studied for years. However, little is known about the vocal communication involved in this behaviour. It has been mentioned that chimpanzees do 'nesting calls' while nesting but no empirical studies have been conducted. This study aims to describe how chimpanzees communicate with each other during nesting and which type of vocalizations are used. To do so, vocal exchanges between wild chimpanzees from the Sonso Community in Uganda, were recorded over several evenings. Some of those records have been analyzed and we are now presenting the first preliminary results. We were able to distinguish five main call types used by chimpanzees during nesting time: hoo, wra, pant, long hoo and panted hoo. We wonder now if some of those call types are more likely to be used individually or in combination. We also observed that chimpanzees often do vocal sequences, which corresponds to a vocal exchange between at least two individuals while nesting. We are now trying to determine by which call type a sequence usually starts, which individuals are more likely to call first and which ones are more likely to reply. We also wonder if the duration of a sequence is linked to the number and or the sex of individuals present.

Poster presentation abstracts

Poster N°65

Spatial learning in desert ants and its value under competition conditions

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Central-place foragers explore their habitat in order to reach food. We let colonies of the individually foraging ant *Cataglyphis niger* search for food in a maze. We did so for 3 tests per day over two successive days and another test after a time interval of 4-20 days. We examined whether the colonies reached food faster, consumed more food and changed the number of workers searching over time, within and between days. Colonies' food-discovery time shortened within and between days. Such workers, however, also forgot and deteriorated in their food-discovery time, leveling off back to initial performance after ~2 weeks. We used mazes of increasing complexity levels, differing in the potential number of wrong turns. The number of workers searching increased with colony size. Food-discovery time increased with colony size in complex mazes but not in simple ones, perhaps due to the more frequent interactions among workers in large colonies having to move through narrow routes. Finally, the contribution of learning to foraging under competition conditions has rarely been tested. We trained colonies to solve either a complex or a simple maze. We then tested pairs of colonies against one another in solving a complex maze and dominating a food reward. The colonies trained in complex mazes solved the maze faster and fed more intensively on the food reward than those trained in simple mazes. Learning may therefore possibly explain the discovery-dominance trade-off of resources.

Poster presentation abstracts

Poster N°66

Ripening physiology of ANNA is modified by preclimacteric events

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Apple (*Malus × domestica*) is a classical climacteric fruit, generating an ethylene burst at the onset of ripening with an increase in respiration. One of the major concerns of apple fruit is their quality loss during storage, affected by ethylene.

We investigated that, an early season apple cultivar "Anna" exhibited fast softening and juiciness loss during storage, in comparison to mid-late season cultivars "Galaxy" and "GD." The poor storage capacity of "Anna" was correlated with high lipid oxidation-related autoluminescence, and high respiration and ethylene production rates, which was associated with high expression of ethylene biosynthesis genes MdACO1, 2, 4, 7, and MdACS1. Moreover, during fruit development "Anna" exhibited auto-stimulatory (system II-like) ethylene response to exogenous ethylene by producing higher ethylene production and respiration rates. The higher ethylene production rate during early fruit development in "Anna" was due to the higher expression of ethylene biosynthesis genes, MdACS3a, MdACO2, 4, and 7. Furthermore, lower expression of negative regulators of ripening (MdAP2/ERF) and ethylene response pathway, (MdETR1, 2 and MdCTR1) and SQUAMOSA promoter binding protein (SBP)-box genes, including MdCNR and MdFUL also affects the "Anna" quality.

In conclusion, this study provides new understanding on poor storage capacity and quality of "Anna", associated with higher ethylene and respiration rates and pre-climacteric system II-like characteristic.

Poster presentation abstracts

Poster N°67

IMPROVING ALPINE PLANT SPECIES DISTRIBUTION MODELS WITH HIGH RESOLUTION REMOTE SENSED SNOW COVER

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Antoine Guisan, University of Lausanne

The pivotal role of snow has since long been recognised as an important parameter shaping species distribution and plant communities. Despite this, it has only rarely been incorporated in plant species distribution models. Here, we developed three snow cover indexes using remote sensing of snow cover in the Western Swiss Alps from Landsat8, Sentinel and Worldview2 satellite images at different resolutions. We examined the changes of model predictive performance when adding each snow index in plant species distribution models based on other environmental variables (topography, climate, soil). When models contained only a few environmental variables the predictive power was significantly increased by the addition of our snow indexes at very high resolution and the magnitude was related to the resolution of the satellite images. However, this was not the case when models included more environmental variables. Snow indexes increased particularly the predictive performance of snow beds as well as anthropogenic meadows and pastures species. As this studied area only shows a reduced range of environmental conditions for the studied species, we therefore suggest that more studies are needed using snow indexes from remote sensing at high resolution over larger areas encompassing larger environmental gradients.

Poster presentation abstracts

Poster N°68

Shape and dynamical consequences of the functional response of *Daphnia magna*

Niklas Niklas Ingvar Paulsson, University of Bern

Poster presentation abstracts

Poster N°69

Territorial Behaviors in Meerkats (*Suricata suricatta*) The Influence of Group Size on Investments

Gina Moergeli, University of Zurich
Bart Kranstauber, University of Zurich
Marta Manser, University of Zurich

The variation of group size, and the deviation of an optimal size in particular, can affect the behavior of the group members. In territorial species, interactions with conspecifics occur, carrying risks, and are best avoided if the chances of winning are low. An assessment and the intimidation of the potential opponents can therefore be crucial for the survival of a group. We investigated the effects of group size on the extent of territorial advertisements and the intensity of intruder assessments in meerkats. Long-term data from the Kalahari Meerkat Project was used to analyze the marking events over 2 years for different group sizes. Further, within 5 months, 8 groups with fluctuating group sizes between 2 and 24 individuals were presented with feces of their neighbors. Besides immediate responses, the meerkat groups' behavioral and movement changes were analyzed in the aftermath of simulated intrusions. Both, the long-term markings and the reactions to the experiment revealed that meerkats of smaller groups showed stronger responses on the individual level, and partially on the group level. Also, it was found that the reaction of the meerkats went beyond the period of their interaction with the presented feces. The increased subsequent vigilance may affect the foraging success of the group members, and they might expend unnecessary energy on increased calling and depositing of marks. Also, changes in movement patterns were detected which may affect territory dynamics.

Poster presentation abstracts

Poster N°70

The genetic basis of pathogenicity evolution in *Z. tritici*

Nikhil Singh, University of Neuchatel

Daniel Croll, University of Neuchatel

Plant genomes encode resistance proteins which trigger immune responses upon recognition of specific pathogen effector molecules. Hence there is opportunity for arms races between plants and pathogens, in which plants evolve to maintain their ability to recognise effector molecules and pathogens evolve to escape this recognition. This results in accelerated evolution of virulence genes in pathogens and resistance gene in plants.

Zyzoceptoria tritici, which causes the wheat disease Septoria tritici Blotch (STB) poses a serious challenge to wheat production in temperate regions throughout the world. The project aims to understand the evolution of pathogenicity in the fungal pathogen, using Genome-Wide Association Studies (GWAS). The basic idea is to use GWAS to map different phenotypes associated with the pathogenicity of the *Z. tritici* under different environmental conditions. Since successful infections of different cultivars in agriculture system likely require a multitude of different traits, this leads to complex selection regimes. Further GWAS is required, which will help in identifying genetic variation for adaptive traits of the pathogen. Furthermore, phenotypic plasticity may play a role in host interactions. Hence, the expression of traits under different environmental conditions should be investigated. The information from new GWAS would be related to the knowledge from previous evolution, genetics, metabolomics and transcriptomics based studies on *Z. tritici* to provide a complete picture for the possible evolutionary mechanism.

Poster presentation abstracts

Poster N°71

A Holistic Model of Biodiversity: Linking Plate Tectonics, Climate Change and Evolutionary Processes

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Despite the general agreement that biodiversity is the result of millions of years of diversification, global spatial biodiversity gradients are most frequently associated to contemporary biotic and abiotic factors such as species interactions, climate and productivity. This is partially because the effects of ancient earth processes on life are more difficult to quantify and keep track off. In order to understand and predict biodiversity patterns, we are developing a macroevolutionary mechanistic model that infers biodiversity patterns from historical range dynamics. Adding on a simple allopatric speciation model that considers past habitats suitability, we now consider, within a single framework, genetic distances mechanism, species interactions (e.g. competition through carrying capacity) and dispersion as well as evolution of trading-off traits. The project integrates reconstructions of paleo-habitats (e.g. plate tectonics and Quaternary glaciations) as background habitat information for the model. The spatial diversification model will provide an important tool for null hypothesis testing and better understanding of the processes of speciation and extinction, which will be contrasted with empirical data. Case studies will include the diversification of tree assemblages (e.g. within the Fagaceae family), marine system (e.g. shallow reef habitat in interaction with another project specific to coral reef system) and alpine plant assemblages.

Poster presentation abstracts

Poster N°72

The role of sex-specific condition dependence in the evolution of sexually dimorphic traits

Patrick Rohner, University of Zurich

Wolf U. Blanckenhorn, University of Zurich

Life history theory predicts a tight link between the extent of sexual dimorphism and sex-specific condition dependence. Assuming that the degree of trait exaggeration mirrors viability costs as well as benefits of the bearer, more sexually dimorphic traits should exhibit a larger between-sex difference in condition dependence. While this has been shown to apply among traits within species, condition dependence and sexual dimorphism are also expected to coevolve across the phylogeny, a prediction that has received little attention. We investigate the relationship between sex-specific condition dependence and sexual dimorphism both within and across 12 species and populations of black scavenger flies (Diptera: Sepsidae). Estimating sex-specific allometric slopes for seven morphological traits that vary greatly in the direction and extent of sexual dimorphism, we 1) find support for a positive relationship between condition dependence and relative trait exaggeration among traits within species, 2) as well as a coevolution across species. Our study suggests a common genetic/developmental basis of sexual dimorphism and sex-specific plasticity that can evolve across the phylogeny.

Poster presentation abstracts

Poster N°73

Genomics of *Microphallus* parasite adaptation to its host, *Potamopyrgus antipodarum*

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Antagonistic co-evolution between host and parasite can be a major force driving genetic variation in both species. Most research on co-evolutionary dynamics has focused on interactions between host and prokaryotic or viral pathogens. Much less evidence for co-evolutionary dynamics comes from interactions between host and eukaryotic pathogen. We study antagonistic co-evolutionary interactions between *Potamopyrgus antipodarum* snail and trematode *Microphallus* sp with the aim to uncover the genomic changes triggering adaptation of parasite to its host. *Potamopyrgus antipodarum* snail is characterized by emergence of common asexual host genotypes that are highly resistant to the parasite. The parasite evolves counter adaptations that render those previously resistant hosts susceptible. Our main goal is to create a reference genome for *Microphallus* sp and compare genomes of the rare genotypes infective to the resistant snails to those infective to host individuals with average susceptibility using full genome re-sequencing. We wish to use the architecture of the genome to discover the signature of local adaptation in the genome and to examine the alternative models of interacting genes of the host and parasite and test the that are predictions relevant for the Red Queen fluctuations maintaining the diversity within the two species.

Poster presentation abstracts

Poster N°74

Disease susceptibility of ant social networks

Alciatore Giacomo, University of Lausanne

Yuko Ulrich, university of Lausanne

According to epidemiological models, the structure of interaction networks has a key role in how a disease can spread in social groups. It has been suggested that social groups might have evolved adaptive behaviour to minimize the risk of epidemics, for example by decreasing the rate of interaction between individuals exposed to pathogens and their nestmates. Living in densely populated, extensively interacting communities, ants are an excellent model to study how different networks affect disease susceptibility and colony resistance to infectious diseases.

I will present preliminary data on interaction networks in small colonies (12-24 individuals) of the clonal raider ant *Ooceraea biroi* obtained using an automated tracking system. The unique biology of this parthenogenetic ant allows me to easily create social groups of arbitrary size and composition. I will describe network properties (i.e. clustering, density or degree heterogeneity) for social groups of different composition. Description of such properties will be useful to predict disease susceptibility of social groups, which will be tested in a further step using experimental infections.

This study system will allow me to study how ant colonies defend against infection and to experimentally test the theoretical epidemiological models based on interaction networks.

Poster presentation abstracts

Poster N°75

The nature of modular connections between traits and their underlying genes affects their rate of adaptation

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Frédéric Guillaume, University of Zürich

Phenotypic traits do not always respond to selection independently from each other and often show correlated responses to selection. The structure of a genotype-phenotype map (GP map) determines trait covariation, which involves variation in the degree and strength of the pleiotropic effects of the underlying genes. It is still unclear, and debated, how much of that structure can be deduced from variational properties of quantitative traits that are inferred from their genetic (co) variance matrix (G-matrix). Here we aim to clarify how the extent of pleiotropy and the correlation among the pleiotropic effects of mutations differentially affect the structure of a G-matrix and our ability to detect genetic constraints from its eigen decomposition. We show that the eigenvectors of a G-matrix can be predictive of evolutionary constraints when they map to underlying pleiotropic modules with correlated mutational effects. Without mutational correlation, evolutionary constraints caused by the fitness costs associated with increased pleiotropy are harder to infer from evolutionary metrics based on a G-matrix's geometric properties because uncorrelated pleiotropic effects do not affect traits' genetic correlations. Correlational selection induces much weaker modular partitioning of traits' genetic correlations in absence than in presence of underlying modular pleiotropy.

Poster presentation abstracts

Poster N°76

Dispersal traits explain diversity contrasts across families and regions in coral reef fishes

Giulia Donati, ETHZ

Valeriano Parravicini, University of Perpignan

Oskar Hagen, ETHZ, WSL

Christian Heine, University of Sydney

Michel Kulbicki, University of Perpignan

Theo Gaboriau, University of Lausanne

Nicolas Salamin, University of Lausanne

Fabien Leprieur, University of Montpellier

Camille Albouy, IFREMER

Loic Pellissier, ETHZ, WSL

Species dispersal is a pervasive force modulating both the ecological and evolutionary processes shaping global patterns of biodiversity. Tropical reef fishes show over ten-fold differences in species richness among clades, but also among tropical regions, which could be conjointly explained by dispersal. We investigate how species dispersal traits together with habitat dynamics through geological times explain the current organization of tropical reef fish assemblages worldwide. We examined whether seven species traits related to dispersal explain diversity contrasts across clades and regions using two complementary approaches. We inferred diversification rates for ten families and related them to dispersal traits through a phylogenetic-based approach, which was compared to a spatially-explicit model where diversification rates are associated to dispersal. Dispersal traits including adult home range and body elongation were strongly negatively associated to diversification rates. Congruent with this result, spatially-explicit simulations with low dispersal parameters spatially matched areas with a large proportion of species with small home range and body size. Taken together, our findings suggest that a set of traits modulating dispersal played a major role in shaping species diversification within clades together with the spatial organization of coral reef fish functional assemblages worldwide.

Poster presentation abstracts

Poster N°77

Eco-evolutionary physiology of environmental stress: does corticosterone facilitate adaptive divergence of the moor frog (*Rana arvalis*) along an acidification gradient?

Jelena Mausbach, Eawag, Aquatic Ecology, ETH Zurich

A Laurila, Eawag, Aquatic Ecology

Katja Räsänen, NA

Physiological processes, as immediate responses to the environment, are important mechanism of phenotypic plasticity and can be crucial for evolution at ecological time scales. Understanding how physiological plasticity mediates adaptation to environmental stress in time and space, aids in predicting evolutionary responses to environmental change. In stressful environments, an individual reacts by releasing stress hormones, such as corticosterone (CORT), which enables energy mobilization to various stress response traits/functions. We investigate whether CORT may be a key mediator of adaptation to environmental stress, such as human induced acidification. The moor frog (*Rana arvalis*) shows adaptive divergence in key fitness traits (embryonic acid tolerance, larval life-histories and predator defenses) along an acidification gradient in Sweden. As a first step towards understanding the role of corticosterone in this adaptation, we conducted a common garden laboratory experiment (rearing of tadpoles at benign, pH 7.5, versus stressful, pH 4.2, conditions). The presentation will provide first insight to whether tadpoles from three phenotypically divergent populations differ in their CORT profiles and CORT-phenotype correlations.

Poster presentation abstracts

Poster N°78

Transcriptome and chromatin dynamics during a population growth of *Tetrahymena thermophila*

Vanessa Weber de Melo, University of Zurich
Robert Lowe, Queen Mary University of London
Paul Hurd, Queen Mary University of London
Owen Petchey, University of Zurich

Ecological and evolutionary processes, ranging from competition to adaptation, are dependent on population density. Despite its relevance, the molecular basis of population responses to changes in density remains poorly understood. To explore this question, populations of *Tetrahymena thermophila*, a unicellular eukaryote well suited to explore genetic and epigenetic mechanisms, were grown from low densities until carrying capacity was reached. Three replicate populations were sampled at three different densities and all samples were analyzed with RNA-seq and ChIP-seq to obtain gene expression and histone modification patterns across the genome. The transcriptomes sampled at increasing population densities revealed 2,599 genes differentially expressed throughout exponential growth but distribution of four different histone modifications appeared inconsistent with gene expression patterns. Nuclei isolation and chromatin immunoprecipitation protocols were optimized for *T. thermophila* to ensure higher quality of ChIP-seq data. A second experiment was performed, sampling *T. thermophila* populations across six different densities and monitoring them with videos, allowing the additional characterization of morphological features. RNA-seq and ChIP-seq samples obtained with the improved protocols are being sequenced and, together with the morphological data, will give a more detailed understanding of the role of gene expression and regulation for density-dependent population dynamics.

Poster presentation abstracts

Poster N°79

The role of differential parasite load and immune system response in adaptive divergence of an East African cichlid fish

Jelena Rajkov, University of Basel

Walter Salzburger, University of Basel

Bernd Egger, University of Basel

The East African cichlid fish *Astatotilapia burtoni* is an emerging model to study adaptive divergence across an environmental gradient. Various lake-stream population pairs exist in Lake Tanganyika and affluent rivers that display different degrees of genetic and morphological differentiation and rest at different stages of the 'speciation continuum'. Genome scans have identified candidate genes with inferred functions in the immune system that show differences in gene expression between lake and stream populations. Here, we investigate an interaction with habitat-specific pathogens and the underlying immunological capabilities of ecotype hosts as a potential factor in lake-stream divergence. To this end, we inspected two lake-stream population pairs and fish from a common garden setup. Screening of guts and gills for metazoan ecto- and endoparasites revealed that lake populations experience higher infection levels and lake-specific parasite taxa. The splenosomatic index showed that, in the wild, lake populations have higher level of innate immune response to parasite infections. Using microbiota analysis from gut and buccal mucosa and differential expression analyses from RNAseq of spleen and gills we aim to investigate habitat-specific microbiota communities and immune related gene expression patterns. Together, these experiments will contribute to a better understanding of the importance of pathogens and immune system response in the divergence of cichlid fishes.

Poster presentation abstracts

Poster N°80

Genetic basis of clownfish adaptive radiation

Anna Marcionetti, University of Lausanne

Victor Rossier, University of Lausanne

Joris Bertrand, University of Perpignan

Nicolas Salamin, University of Lausanne

Clownfishes (family: Pomacentridae) is a group of 28 described species and their distinctive characteristic is the mutualistic interaction they maintain with sea anemones. This mutualistic interaction was identified as the main -key innovation- that opened new ecological niches and triggered the adaptive radiation of clownfishes. Little is known about the genetic mechanisms that allowed clownfishes to adapt to their sea anemones hosts. There is also very little understanding of the process that led to the diversification of the clownfishes once they acquired the mutualistic interaction. Thanks to the advances in next generation sequencing technologies, we are investigating the genomic basis of the diversification process of the clownfishes.

We sequenced, assembled and annotated the genomes of 10 clownfish species. We used comparative methods and models of molecular evolution to infer the level of selection on all the one-to-one orthologous genes of the clownfishes and on clownfish-specific duplicated genes. We identified few genes under positive selection that are potentially associated with the adaptation of clownfishes to sea anemones and their diversification. These preliminary results suggest that at its early stages, this adaptive radiation was triggered by changes in few genes of large effect and our findings corroborate the expectations from theories of adaptive radiation.

Poster presentation abstracts

Poster N°81

Genetic basis of a key speciation trait in cichlids

Anna Fiona Feller, University of Bern & Eawag

Ole Seehausen, University of Bern & Eawag

Adaptive radiation describes the process of rapid diversification of a single lineage into an array of many ecologically varied species. The cichlid adaptive radiation of Lake Victoria comprises over 500 species that have evolved in the lake within 15 k years. In addition to some environmental characteristics, sexual dichromatism has been shown to be an important predictor for whether a cichlid lineage radiates or not. Male color may thus be one key trait in this radiation. In closely related species pairs of the genus *Pundamilia*, divergence in male nuptial color and female preferences have been shown to be associated. Additionally, they both correlate with divergence in underwater light regimes and differentiation in visual systems, indicating that reproductive isolation by female mate choice in this system likely arose as by-product of a sensory drive process. In the young sister species pair *Pundamilia* sp. 'nyererei-like' and *Pundamilia* sp. 'pundamilia-like', males differ strikingly in color, with males of *P.* 'nyererei-like' being predominantly red and yellow, and males of *P.* 'pundamilia-like' being predominantly blue. Previous studies have estimated few genes (with epistatic and dominance effects) to underlie the difference in red and yellow coloration between the two species. Using Quantitative Trait Locus (QTL) mapping approaches, this study aims to further test these estimates and investigate the genetic architecture underlying this potential key speciation trait.

Poster presentation abstracts

Poster N°82

Abandoning the ship using sex, dispersal, or dormancy: multiple escape routes from challenging conditions.

Nina Gerber, University of Zürich

Hanna Kokko, University of Zürich

Natural populations often experience environments that vary in space and over time, leading to spatiotemporal variation of the fitness of a genotype. If local conditions are poor, organisms can disperse in space (physical movement) or time (dormancy, diapause). Facultative sexual organisms can switch between asexual and sexual reproduction, and thus have a third option available to deal with maladaptedness: They can engage in sexual reproduction in unfavourable conditions (an 'abandon-ship' response). Sexual reproduction in facultatively sexual organisms is often coupled with dispersal and/or dormancy, while bet-hedging theory at first sight predicts a negative relationship, as different escape mechanisms could substitute for each other. Here we briefly review the observed links between sex, dormancy and dispersal, and model the expected covariation patterns of dispersal, dormancy and the reproductive mode in a context of local adaptation to spatiotemporally fluctuating environments. The sign of correlations between sex, dormancy and dispersal evolve to be different in within-species vs. across-species patterns. Various risk-spreading strategies are not completely interchangeable, as each of them has dynamic consequences that can feed back into the profitability of another. Our results shed light on the discrepancy between theoretical predictions on covarying risk-spreading traits and help explain why sex often associates with other means of escaping unfavourable situations.

Poster presentation abstracts

Poster N°83

Constructing a linkage map for Swiss Alpine whitefish

Rishi De-Kayne, University of Bern/EAWAG

Ole Seehausen, University of Bern/EAWAG

Philine Feulner, University of Bern/EAWAG

Knowledge about genomic differentiation between species within an adaptive radiation contributes to a better understanding of the role of ecological speciation in creating biodiversity. The recent origin and repeated diversification of fish in post-glacial lakes provides an ideal system in which to study the genomic changes underpinning ecological diversification. Within the Alpine whitefish (*Coregonus spp.*) species complex, the radiations of six or more sympatric species of whitefish in some lakes are thought to have been facilitated by ecological and reproductive strategy differentiation with sympatric species varying in diet, body length, gill-raker number and spawning depth. The first step towards building genomic resources to better understand the genomic changes underpinning speciation in this system involves the production of a linkage map. We produced F1 offspring by crossing two wild whitefish from Lake Thun in Switzerland. Both parents and over 120 offspring were genotyped using a RAD approach, resulting in a male and a female linkage map each with ~900 SNP markers. I will describe the structure of the linkage map and the identified synteny of genomic regions between whitefish and other salmonid species. In the future this linkage map will aid in the construction of a reference genome for the whitefish.

Poster presentation abstracts

Poster N°84

Non-genetic paternal effects in a species with no paternal care

Valérian Zeender, Universität Zürich

Jhoniel Perdigón Ferreira, Universität Zürich

Hayat Mahdjoub, Universität Zürich

Jeannine Roy, Universität Zürich

Sonja Sbilordo, Universität Zürich

Stefan Lüpold, Universität Zürich

Recent theory predicts that developmental conditions during early-life stages not only affect male health and fitness, but that these effects can also be transmitted non-genetically to the offspring. Such non-genetic inheritance can overcome some limitations of genetic inheritance and is a potentially important process underlying adaptations to rapid environmental change. However, unlike the well-studied maternal effects influencing offspring quality, much less is known about non-genetic paternal effects, particularly when the paternal investment in offspring is limited to transferring ejaculates.

In order to disentangle the non-genetic paternal inheritance from genetic inheritance and direct effects of the larval environment, we reared different *Drosophila melanogaster* isogenic lines either under standard or restricted food conditions across two generations and measured in each generation the sex-specific health and fitness in a series of assays.

We observed an effect of larval condition and genetic background on the development and fitness of flies of the second generation. In addition, the development and fertility of females, but not that of males, seemed to be influenced by the developmental conditions experienced by their sires, indicating sex-specific transmission of non-genetic paternal effects. These effects may have important consequences for the evolution on health- and fitness-related traits.

Poster presentation abstracts

Poster N°85

Cell-level life history trade-offs under cancer risk

E. Yagmur Erten, University of Zurich

Hanna Kokko, University of Zurich

Cooperation between cells is fundamental for multi-cellularity. In a multi-cellular organism, most stem cells divide as part of their role in somatic maintenance rather than to reproduce. However, each division occurs with a probability of mutations that could lead to 'defection' allowing uncontrolled growth, which could ultimately cause cancer. More divisions then mean an increased mutational load and consequently a higher probability of cancer. How do multi-cellular organisms make sure to rid themselves of the 'bad' cells that can cheat and start to proliferate at their own interest, without depleting their stem cell pool too fast? Here we present a model of tissue dynamics, where we study the division and differentiation processes during growth and somatic maintenance and investigate optimal cell-level strategies with respect to apoptosis rules, telomere length and tissue structure. Our ultimate aim is to relate the insights from our cell-level model to the level of the organism, creating predictions for species differing greatly in body size.

Poster presentation abstracts

Poster N°86

CRISPR-Cas9 induced mutagenesis in threespine stickleback (*Gasterosteus aculeatus*)

Matthew Josephson, University of Bern, Institute of Ecology and Evolution

Catherine Peichel, University of Bern, Institute of Ecology and Evolution

Threespine stickleback (*Gasterosteus aculeatus*) fish have invaded freshwater thousands of times since the last glacial maxima, giving rise to numerous populations that have independently adapted to freshwater. Marine and freshwater sticklebacks differ dramatically in morphology, physiology and behavior. Previous genetic mapping and gain-of-function studies have shown that at least three phenotypic differences between marine and freshwater sticklebacks (lateral plate number, neuromast pattern, and schooling behavior) are regulated by expression of a gene called *Eda*. However, it is not known which genetic changes in the *Eda* locus control these traits, or whether these phenotypes are controlled by a single pleiotropic mutation or by several linked mutations. Thus, we are using a CRISPR-Cas9 based genome editing approach to change individual polymorphisms in the *Eda* locus between the marine and freshwater ecotypes to determine if they are involved in evolution of these traits. Here we present a workflow for injecting stickleback embryos with Cas9 mRNA and a guide RNA that is able to efficiently generate insertions and deletions (indels) at the *Eda* locus. Induced indels are primarily small deletions, consistent with previous work. These data suggest that CRISPR-Cas9 can be used to knock-out gene function in stickleback. Further experiments aim to optimize efficiency of CRISPR-Cas9 in stickleback, and develop homology directed repair methods for genome editing in stickleback.

Poster presentation abstracts

Poster N°87

Molecular phylogenetics of barn owls (Tytonidae) using Hybridization RAD Sequencing

Uva Vera, University of Lausanne

Tomasz Suchan, Institute of Botany, Polish Academy of Sciences

Luca Fumagalli, University of Lausanne

Alexandre Roulin, University of Lausanne

The owl family Tytonidae comprises 16 species assigned to two genera. Based on the most comprehensive sampling to date (14 species), and a multi-locus approach using seven mitochondrial and two nuclear markers, taking advantage of field data and museum collections available worldwide, we have established a probable origin of the family in the Middle Eocene (ca. 44 mya) of Australasia. Although we were also able to establish species relationships, and confirm previous findings that the Common Barn-owl 'Tyto alba species complex' is divided into three species, we concluded that for estimating subspecies relationships, and detailed colonisation scenarios of the family, with a high degree of certainty, this sanger sequencing approach still fell short, particularly due to our use of degraded DNA samples from museums. In the recent years, many RAD-sequencing protocols have been adapted to processing museum samples, including a novel method called hybridization RAD (hyRAD) sequencing, that addresses several issues with other museum-adapted approaches. Given that the application of this method does not rely on restriction site presence, it is not sensitive to among-sample loci polymorphisms in the restriction sites that usually causes loci dropout. This enables the application of hyRAD to analyses at broader evolutionary time scales. Here, we applied this method to 276 samples of the family Tytonidae, and present preliminary analysis and results.

Poster presentation abstracts

Poster N°88

Well-behaved transposable elements despite drastic demographic changes in the Mediterranean grass *Brachypodium distachyon*

Michele Wyler, University of Zurich

Anne Roulin, University of Zurich

Poster presentation abstracts

Poster N°89

Using ADME genes to explore modern human evolution between Africa and Eurasia.

Médéric Mouterde, University of Geneva
Youssef Daali, Geneva University Hospitals
Victoria Rollason, Geneva University Hospitals
Sotiria Boukouvala, Democritus University of Thrace
Said Al-Yahyaee, Sultan Qaboos University
Getnet Yimer, Addis Ababa University
Viktor Černý, Charles University of Prague
Jules Desmeules, Geneva University Hospitals
Estella S. Poloni, University of Geneva

Why some people can take a medication at a standardly prescribed dose when it can cause dangerous side effects to others? Numerous factors participate to this phenomenon, one of them being genetics. On the basis of such undesired effects observations, physicians have made an inventory of genes involved in the absorption, distribution, metabolism, and excretion of drugs, which they have pooled together in a group of genes called ADME. From an evolutionary point of view, ADME genes are interesting because they are potential targets of ancient or recent selection in humans, resulting from adaptations to new chemical environments, diets or lifestyles during modern humans' history. Under this assumption, the goal of our project is to identify differentiated patterns of diversity between populations, and determine whether they result from adaptive or demographic processes.

We sampled 361 individuals in 4 countries located between East Africa and West Eurasia, (Czech Republic, Greece, Oman and Ethiopia) that were genotyped with a genome-wide 550K SNP array and phenotyped for their physiological responses to 7 compounds, and we present here our first results. By exploring differences between ADME genes and the rest of the genome with discriminant analyses and structure analyses, we present different patterns and differences that could be signals of adaptations or marks of demographic processes.

Poster presentation abstracts

Poster N°90

Cichlidogyrus parasitic infection and its potential role in the diversification of its cichlid fish host

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Maarten PM Vanhove, Masaryk Uni, KU Leuven, Hasselt Uni, Helsinki Uni
Ton GG Groothuis, University of Groningen
Martine E Maan, University of Groningen
Ole Seehausen, University of Bern, EAWAG

Parasites and hosts may engage in arms races, potentially promoting the divergence of host populations exposed to different parasites.

In Lake Victoria, cichlids have undergone adaptive radiation, resulting in a wide ecological. They are infected by *Cichlidogyrus*, a species-rich genus of monogenean worms that is specific to cichlids and exhibits host specificity in some cichlid lineages.

We investigate the contribution of *Cichlidogyrus* to Lake Victoria cichlid speciation, by testing: 1) if different host species have different infection profiles, that would emerge from the evolution of specific resistance; 2) for host-parasite co-diversification, as opposed to sorting of ancestral *Cichlidogyrus* species among newly arisen host, by including a host lineage that is not part of the radiation. We predict a higher worm diversity and abundance in the non-diversified lineage, as it may not have evolved specific resistance.

Cichlidogyrus were isolated from the gills of 6 sympatric endemic cichlid species: the non-diversified *A. alluaudi* and 5 species of the radiation. Worm morphology was assessed to identify morphospecies.

Infection profiles were similar in all 5 radiating cichlids, inconsistent with parasite-driven diversification. The non-diversified host had more worm individuals and morphospecies. These results suggest that parasite resistance differs between radiating and non-radiating species, but do not support a role of parasites in driving divergence within the radiation.

Poster presentation abstracts

Poster N°91

Repeatability of genomic evolution across multiple adaptive radiations

David Marques, University of Bern & Eawag

Ole Seehausen, University of Bern & Eawag

Whether replaying the tape of life would result in similar phenotypes or not has been a longstanding debate in evolutionary biology. Examples for convergent or parallel evolution, when organisms adapt in a similar way to similar selective challenges, suggest that evolution is indeed often deterministic on the phenotypic level. However, we usually do not know whether the same pathways, the same genes, amino acid changes or mutations are involved. There is also little empirical insight on how the genomic architecture of traits influences the repeatability of evolution. We investigate the genetic basis of repeatedly evolved phenotypes in multiple adaptive radiations of haplochromine cichlids in the Lake Victoria region using whole genomes, GWAS-like approaches and functional analyses. All radiations evolved from a hybrid swarm between two divergent lineages, allowing us to assess when evolution from a common starting point is repeated at the genetic level. We will present preliminary data on the genetic basis of traits under natural and sexual selection and ask how genomic architecture influences evolutionary repeatability.

Poster presentation abstracts

Poster N°92

Modularity Buffers the Spreading of Cheaters in Social Networks

Daniel Wechsler, University of Zurich

Jordi Bascompte, University of Zurich

A major scientific challenge is to identify the mechanisms that can explain the ubiquity of cooperation in nature in light of its vulnerability to exploitation. It is known that population structure can constitute such a mechanism, because non random interactions allow cooperative individuals to cluster together and prevail by mutually benefiting each other.

Here, we study evolutionary games on modular networks to understand the effect of a modular population structure on the resilience of a cooperative community against the invasion of defective individuals. We find that the fraction of modules being invaded when starting from a single invasive defector undergoes a non-linear transition as network modularity increases.

In particular, this effect is only observed if modularity exceeds a certain critical threshold value. This critical value is at the local scale determined by the probability that defectors manage to transcend to adjacent communities before reaching a critical local density.

Agreement between simulations and a mathematical approximation indicates that, at the global scale, the critical threshold corresponds to the epidemic threshold in a certain class of disease spreading models.

Poster presentation abstracts

Poster N°93

Effect of copulation on longevity in the male black scavenger fly *Sepsis punctum* (Diptera: Sepsidae) across different environments

Ramon Dallo, ETH Zürich

Patrick Rohner, University of Zurich

Oliver Martin, ETH Zürich

It is well established that copulation can be costly for female insects by decreasing longevity, yet comparable costs to males are comparatively poorly studied. Such costs may further be affected by the environmental conditions experienced by males. We investigated the effect of the number of copulations on male longevity across environments in two distant populations of *Sepsis punctum*. We used an European and an American fly population, which have contrasting mating behaviors. The European population shows male-male competition for access to mates, while the American population shows elaborate courtship behaviors. Males of each population were assigned a priori to three different copulation treatments. Males could copulate once or twice and were compared to a control group of virgins. In addition to varying the number of copulations, we also manipulated the environment after the mating treatments. One third of all males was kept in a control treatment with access to ample amounts of food while a second group underwent a starvation treatment. Thirdly, we also exposed males to food spiked with ivermectin, a widely used veterinarian pharmaceutical with known negative effects on insects. We expect males to suffer from viability costs with increasing number of copulations and further predict these costs to vary across environments. We discuss potential drivers of variation in male copulatory costs and the role of environmental variation in shaping reproductive investments.

Poster presentation abstracts

Poster N°94

Population genomics of island barn owls (*Tyto alba*)

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Alexandre Roulin, Department of Ecology and Evolution, University of Lausanne

Jérôme Goudet, Department of Ecology and Evolution, University of Lausanne

The evolutionary mechanisms that drive and maintain variation within and among species have long fascinated biologists. The recent technological advances in whole-genome sequencing have boosted this field by generating large scale data and thus addressing new questions. Specifically, one can now attempt to disentangle the roles of demographic history and natural selection in the intraspecific genetic and phenotypic diversity. As the classical example of the adaptive radiation of Darwin's finches illustrates, islands are suitable study systems to address such questions, with implications on the understanding of evolutionary processes. The widespread barn owl (*Tyto alba*) displays remarkable geographic variation in plumage coloration. Here, we study the population structure and demographic history of island barn owl populations as well as the evolutionary processes underlying their phenotypical divergence from their mainland counterparts. Population genetics analyses with microsatellite data, indicated that neutral genetic differentiation between islands and mainland is higher than what was expected for such a mobile organism. To further investigate these neutral patterns as well as the genetic basis of colour variation, we have re-sequenced the full genomes of roughly 100 individuals across continental and insular Europe. We present preliminary results of population genomics analyses for Great Britain, Ireland and Crete.

Poster presentation abstracts

Poster N°95

Population genomics of the Barn Owl around the Mediterranean

Guillaume Dumont, University of Lausanne

Alexandre Roulin, University of Lausanne

Jérôme Goudet, University of Lausanne

Studying populations at an early stage of differentiation can bring great opportunity to understand mechanisms at the origin of this phenomenon of divergence leading potentially to speciation. The barn owl exhibits a marked color polymorphism across the Western Palearctic that seems to be associated with some interesting genetic and demographic features. Particularly, a previous genetic study based on 20 microsatellite suggested the colonization of the region in a ring like manner around the Mediterranean ending with a potential contact zone in the Balkans between the two color morphs. To study this more deeply, we sequenced the whole genome of 87 individuals in the Balkans and across the area resulting in a data set of more than 15 million SNPs. I will present a first analysis of this dataset, suggesting that genomic patterns may not match the previous genetic results. Particularly, this genomic data shows different origins of the hybrid zone and potentially a new one. These new results bring into question the evolutionary history of the barn owls in the region which we will address through demographic simulations.

Poster presentation abstracts

Poster N°96

Genome-wide expression analyses to dissect the genetic basis of gene regulation in a fungal pathogen of wheat.

Leen Nanchira Abraham, University of Neuchatel

Daniel Croll, University of Neuchatel

Zymoseptoria tritici is a fungal pathogen of wheat causing *Septoria tritici* blotch (STB) which is causing serious yield loss globally. Studies on natural populations of this pathogen showed substantial variation in gene expression among isolates which can confer an adaptive advantage. Gene expression is regulated at different time points with several proteins. The close proximity of transposable elements (TEs), epigenetic modulators and histone proteins with genes suggested the involvement of these elements in gene regulation. A population-wide association mapping and transcriptomics on natural population of *Zymoseptoria tritici* can identify regulatory polymorphisms associated with genes. The regulatory elements mapped through expression GWAS (eGWAS) will be categorized in to *cis* and *trans* based on the distance from their gene of action. Analysis of fold change of gene expression between *in vitro* and *in planta* cultures of *Zymoseptoria* will identify the genes primarily involved in the infection process and its regulatory elements.

Poster presentation abstracts

Poster N°97

Missing X chromosome leads to a deficiency in male function

Xinji Li, University of Lausanne

Paris Veltsos, University of Lausanne

Guillaume Cossard, University of Lausanne

Jörn Gerchen, University of Lausanne

John Pannell, University of Lausanne

The annual plant *Mercurialis annua* is considered to have homomorphic XY chromosomes, which are indistinguishable under the microscope. Genomic studies find few X- or Y-specific sequences. We assess the level of Y chromosome degeneration by growing individuals containing two copies of Y chromosomes, established by hormone feminization and pruning treatment. We find no difference in viability or morphology between XY and YY individuals. However, crossing experiment suggests partial sterility in YY, contrast to the expectation of 'supermales' with an extra Y chromosome to accumulate male fertility genes. SEM and TEM observations show differences in pollen shape and ultrastructure. The cytoplasm of the pollen produced by YY males is necrotic without reserves of starch, compared to that of XY. We discuss potential reasons to retain male fertility factors on the X chromosome.

Poster presentation abstracts

Poster N°98

Revelations about the mysterious intimacy of bats

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Males of the genus Vespertilionidae (Chiroptera) have the ability to separate the costs of spermatogenesis from those generated by the search for sexual partners. In addition, sperm storage by females extends the mating period, and thus allows numerous males to copulate with them. In this context of extreme sperm competition, any attribute enhancing male fertility should be strongly selected. In the past years, we studied the anatomy of the erected penis, the morphology of spermatozoa and sperm mobility in several sperm storing bat species. Our results underpin the occurrence of strong selective pressures. These forces might have shaped a variety of forms and structures that were, until now, unsuspected. This work further aims at better understanding the still elusive intimacy of bats.

Poster presentation abstracts

Poster N°99

Adaptive response to novel conditions: a potential biocontrol agent as model system

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Accidental introductions offer unprecedented bio-geographical experiments to study on-going evolutionary processes, such as rapid adaptive responses to novel conditions. As a potential biocontrol agent of the invasive weed *Ambrosia artemisiifolia*, the leaf beetle *Ophraella communa*, recently and accidentally introduced in Europe, offers an interesting case to study such processes. Native to North America, the beetle is currently considered as an effective biocontrol agent in China but because it's an oligophagous species, its potential benefit and risks urgently need to be assessed before its use as a biocontrol agent in Europe. To explore the potential for adaptation to both biotic and abiotic factors, we investigate the response of the beetle to different plants and temperature regimes in populations sampled both from its native and introduced ranges, and along latitudinal and altitudinal gradients. Our studies will shed light on the phenotypic divergence among populations in different ranges, discriminate between phenotypic plasticity and genetic differentiation, and finally explore phenotype-environment associations in view of testing for the potential of adaptation in the introduced ranges. Currently, larval performance has been evaluated in our quarantine facilities on four populations from China. Preliminary results show different survival among populations and families and that this was rather affected by temperature than by plant species.

Poster presentation abstracts

Poster N°100

Towards a global phylogeography of the Asian tiger mosquito

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The Asian tiger mosquito (*Aedes albopictus*) is one of the most invasive species on this planet. It is an important vector of the Dengue, Chikungunya and potentially Zika viruses. Despite the considerable research effort in the past it is not yet fully understood along which routes this species spreads and which genetic lineages contribute to its successful global invasion.

Invasions are characterized by newcomers representing only a subset of the genetic diversity of the source population. Hence, it is possible to assess the population of origin by using genetic markers. However, in the case of *Aedes albopictus* the introduction history is complex due to multiple introduction events from different sources. Sequencing the whole genome using ddRAD provides a tool to obtain sufficient resolution to determine source populations and the connectivity between populations of the native and the invasive range. In addition these data will allow distinguishing recent and historical introduction events. This way we will reveal the overall global dispersal patterns that gave rise to the regional invasions revealed by earlier studies.

Here, I will present a project that has recently been launched to understand the global dispersal patterns and routes of invasion of the Asian tiger mosquito.

Poster presentation abstracts

Poster N°101

On potential causes of inter-individual variation in cooperation by the bluestreak cleaner wrasse, *Labroides dimidiatus*

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While variation between individuals might be essential for the evolutionary maintenance of cooperation, few empirical studies try to assess inter-individual variation in a cooperative system and its underlying causes. We started to tackle these issues in a study on the blue streak cleaner wrasse and its 'client' reef fishes. Clients come to cleaning stations to have their ectoparasites removed. However a conflict of interest arises because cleaner fish prefer to eat healthy tissue from clients rather than their parasites. We first filmed 32 cleaner fish, on 3 occasions, interacting with clients in the wild and extracted client jolts as a correlate of cheating by cleaners. We then captured these individuals and brought them to lab where we measured their standard and maximum metabolic rate, general activity, responses to novel objects and to a mirror, and cognitive performance in ecologically relevant tests. Behavioural and physiological traits were repeatable across time, including the frequency of cheating in the wild (all $R_s > 0.15$). Cleaners that were more exploratory were more prone to cheat their partners. Variation in other behaviours (activity rate, reaction towards reflection in a mirror and cognitive abilities) and in metabolism (SMR, MMR) had no effect on cleaners' cheating frequency. In summary, our study suggests that cleaners' levels of cooperation in the wild are rather independent of individual characteristics such as metabolism or cognitive abilities.

Poster presentation abstracts

Poster N°102

QTL analysis of parasite resistance in *Daphnia magna*

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Coevolution between parasites and their hosts plays an important role in creating and maintaining the world's biodiversity. Revealing the genetic mechanisms of these dynamic interactions can help us understand the evolutionary forces that drive them. The Red Queen hypothesis predicts that under certain conditions of host-parasite coevolution, diversity in the host population is maintained by negative frequency-dependent selection, which favors rare alleles and results in cycling patterns of allele frequencies. This theory has been invoked to explain the variation in susceptibility of the crustacean *Daphnia magna* to its bacterial parasite, *Pasteuria ramosa*. However, before the Red Queen hypothesis can be formally tested in this system, the alleles under selection must be identified. In the present study, we conduct a QTL analysis to investigate the genetic basis of *D. magna*'s resistance/susceptibility to one genotype of *P. ramosa*. The results will add to an existing genetic model that includes five interacting loci and is based on previous work that analyzed resistance to four additional *P. ramosa* genotypes. This work will bring us closer to our goal of testing the Red Queen hypothesis, and it will contribute to a broader understanding of the genetics of host-parasite interactions.

Poster presentation abstracts

Poster N°103

Reversal learning tasks in crib-biters and non-stereotypic horses

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Stereotypies in animals are a consequence of captive environment. Following frustrated situations, animals may stay in chronic stress states, resulting in sensitization of a brain area, the basal ganglia. Due to its primary role, dysfunctions of the basal ganglia can lead to altered learning performance. To assess the presence of such an alteration, cognitive tests have been developed in animals. The aim of this study was to investigate potential alterations of the dopaminergic system in stereotypic horses (crib-biters, CB) and non-stereotypic horses (controls, C). To this aim, six CB and seven C horses were subjected to two discrimination reversal tasks using visual cues. In addition, heart rate (HR) and HR variability were recorded continuously. All 13 animals completed four phases, i.e. first and second acquisition (Acq1, Acq2), and their reversals (Rev1, Rev2). We did not find any difference in the number of trials needed per phase between groups. Post-hoc comparisons showed that horses needed significantly more trials for Rev1 than for all other phases and performed Rev2 in fewer trials than Rev1, suggesting that they learned to learn. Regarding stress parameters, we did not find any group or phase effect on either HR or HR variability. We conclude that our results do not support the hypothesis that crib-biters may have altered dopaminergic system, and furthermore that horses might be able to perform reversal learning using visual cues.

Poster presentation abstracts

Poster N°104

Experimental effect of a coccidian infection on the soma versus germline oxidative balance and on sperm performance

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Alfonso Rojas Mora, University of Neuchâtel
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Helfenstein Fabrice, University of Neuchâtel

Males have been selected to maximize both mating and fertilization success and therefore face a resource allocation trade-off between pre- and post-mating traits. Oxidative stress has been hypothesized to mediate this trade-off through the soma/germline oxidation trade-off hypothesis, which posits that males should differently invest antioxidant protection in soma vs. sperm according to their social status.

To test this hypothesis, we experimentally infected wild-caught house sparrows *Passer domesticus* with *Coccidia Isopora sp.*, a bird internal parasite that depletes antioxidant resources, to test the hypotheses that (i) males differentially invest their antioxidant resources into their soma vs. their germline according to their social rank, and (ii) that the condition-dependence of sperm performance is mediated by oxidative stress.

Our experimental parasite infection did not affect sperm performance, oxidative stress, or the soma/germline oxidative ratio. However, males generally shifted their soma/germline oxidative ratio towards oxidative protection of sperm while sperm performance generally increased with time. In addition, males at the lower end of the social hierarchy generally had lower sperm velocity. Our study shows that immunity does not necessarily affect sperm performance and oxidative stress but social hierarchy and the soma vs. germline oxidative balance are determinants of male sperm performance.

Poster presentation abstracts

Poster N°105

Can flexible male courtship displays be maintained through sexual selection?

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Tim Fawcett, University of Exeter

Sexual selection theory has focused almost exclusively on the evolution of morphological sexual traits in males, which are assumed to be fixed and displayed to all females to the same extent. This theory does not apply well to behavioural traits, which could be flexibly adjusted from moment to moment and seem to play an important role in mate attraction in many species. It could be argued that if the display level does not consistently reflect the quality of the male, females should evolve to ignore it. To investigate sexual selection on such behavioural courtship displays, we built evolutionary computer simulations in which male courtship strategies coevolve with female preferences. Higher courtship effort may be attractive to females, but it is less likely to result in a mating if there are many competitors also displaying at a high level, and it may also attract predators. The simulations show male investment in flexibly adjusted behavioural courtship effort is stable only when a female preference for more intense courtship is fixed in the population, both in models based on classical Fisherian 'runaway' sexual selection and good genes sexual selection. However, when the female preference is not fixed, it evolves to zero which leads to the loss of male courtship effort. We discuss the conditions under which male courtship effort could be maintained as a target of the female preference.

Poster presentation abstracts

Poster N°106

Sex and parasites: how host-parasite dynamics can influence the maintenance of sex

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Darren J. Parker, University of Lausanne

Choe Larose, University of Lausanne

Tanja Schwander, University of Lausanne

Asexual reproduction presents much more reproductive potential than sexual reproduction: it has a demographic advantage, avoids most costs related to mating, and can maintain favourable combination of alleles. All this considered, why isn't asexual reproduction more common in animals?

Here we test the prediction that asexual populations are rare because they are associated with a lower rate of adaptation, in comparison with sexual populations. Ever-changing environments favour different combinations of alleles over time, and consequently sex. One biotic factor that is able to promote rapid environmental changes is parasite pressure. Indeed, the 'parasite hypothesis for sex' (or the 'Red Queen effect') is one of the most widely accepted hypothesis to explain the rarity of asexual reproduction in nature.

To test the 'parasite hypothesis for sex' we focus on the point of action of host-parasite interactions, the immune defense genes (IG). We use a genus of stick insects (*Timema*) to analyse the effect of the reproductive mode on the evolutionary rates of IG: if host-parasite dynamics are relevant for the ubiquity of sex in nature, then we expect IG to evolve adaptively at a faster rate than the genomic average, when comparing sexual to asexual organisms.

Poster presentation abstracts

Poster N°107

How do cribellate orb-weavers avoid adhering to their web? Testing for an anti-adhesive surface coating in *Uloborus plumipes* (Araneae, Uloboridae)

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Stefan Bachofner, bamutec GmbH, Bachofner Museumstechnik, Hinterkappelen

The cribellate spider *Uloborus plumipes* does not adhere to its web when it touches the capture spiral with any body part. We tested for an organic surface coating with protective properties that had been suggested before for araneid orb weavers. We pulled legs of *U. plumipes*, either untreated ones, or legs washed with an organic solvent (CS₂) or with purified water, and legs of house crickets (*Acheta domesticus*) off a cribellar thread of a web of *U. plumipes* and measured indirectly the strength of adhesion. We found that spider legs adhered significantly less to the capture thread than cricket legs, suggesting a protective mechanism in the spiders. We found no difference in the strength of adhesion between any of the experimental groups of spider legs and therefore conclude, that the spider's protective mechanism must be something different than an organic surface coating.

Poster presentation abstracts

Poster N°108

X-Y differentiation is lineage-specific in Swiss populations of *Rana temporaria*

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Nicolas Rodrigues, University of Lausanne

Alexandra Jansen van Rensburg, University of Zurich

Nicolas Perrin, University of Lausanne

Sex chromosomes are a common sex determination mechanism, but even closely related species may not have homologous sex chromosomes. Most frogs have sex chromosomes that are homomorphic but which may still show signs of genetic differentiation. In the common frog (*Rana temporaria*), both XX and XY males occur, and the degree of X-Y genetic differentiation varies both between and within populations. We genotyped adult and juvenile samples of *R. temporaria* collected across Switzerland at markers within the candidate sex-determining region and across the rest of the sex chromosome. Two distinct Y lineages are present in Switzerland, which differ in their propensity to be differentiated from the X. Moreover, X-Y differentiation is lineage-specific, it is common in one Y lineage but uncommon in the other. The distribution of the two Y lineages is dictated by geography, one is found on each side of the Alpine ridge bisecting Switzerland. This distribution pattern is largely congruent with mitochondrial lineage distributions in Switzerland. These results suggest that differences in Y lineage distribution and sex chromosome differentiation may be a consequence of differentiation due to previous geographic isolation within *R. temporaria*.

Poster presentation abstracts

Poster N°109

Amphipods of Switzerland

Roman Alther, Eawag & University of Zurich

Florian Altermatt, Eawag & University of Zurich

Amphipods are keystone species in many freshwater ecosystems. But although their ecological importance is recognized, the actual diversity and distribution is still poorly studied in many areas, particularly in Switzerland. Up to now there exists neither a detailed overview of all amphipod species from the region, nor an identification key covering all present drainage areas. Over the last few years we collated an extensive database on amphipods of Switzerland. It covers more than 1,800 sites and more than 180,000 identified amphipod specimens. The data originate from various sources, such as the governmental biodiversity monitoring program and reports, published literature and our own extensive sampling. Here, we present the results as distribution maps of all present species of Switzerland. Additionally we updated the checklist of Swiss amphipods from Altermatt et al. (2014). Over the last 150 years, 44 species were recorded in Switzerland. 23 of these were subterranean species, and another 13 species should be considered non-native to Switzerland. A 'Fauna Helvetica' monograph on Swiss amphipods is in preparation and will be published soon.

Poster presentation abstracts

Poster N°110

Pioneers from the continents - molecular phylogeny of the Vitrinidae of the Macaronesian Islands

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The study of isolated islands, considered as biological hotspots and evolutionary engines, was always of distinguished interest to biogeographers. The relationship between Macaronesian and the nearby Mediterranean basin fauna implies interesting questions for the endemic terrestrial snail fauna, notably questions on dispersal abilities as well as colonization mechanisms. My project focuses on the terrestrial pulmonate gastropod family, the Vitrinidae. The Vitrinidae represent a curiosity among the terrestrial molluscs: being half slugs with translucent shells, consisting of widespread species, but also none the less fewer endemics living in extreme climatic conditions throughout the European/African Palearctic realm. Here we show the first molecular phylogeny of the Canarian and Madeiran Vitrinidae opposed to the East African members of the family, generated by a five-gene marker approach, which represents a novelty. It is the first stepping stone to the future exploration of the biogeographical aspects of the Macaronesian islands colonisation patterns, emigration, dispersal and situation of source populations using the family Vitrinidae. In future projects, we will try to reveal the evolutionary life history of the family from the Macaronesian and Mediterranean area, resolving questions of potential immigration pathways through Europe covering a timescale of 68 ma, which represents the maximum age of colonisable land patches in the area.

Poster presentation abstracts

Poster N°111

Phylogenetic reconstruction and species delimitations in relict tree genus *Pterocarya* (Juglandaceae) based on RAD-seq and morphological data sets

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Pterocarya (Juglandaceae) is a riparian relict tree genus with 6 to 8 extant species. Previous phylogenetic studies have failed to establish the stable topology of the genus. Here, we resolve the phylogeny and taxonomy of *Pterocarya*, using next-generation sequencing of restriction-site associated DNA (RAD-seq) and analyses of plant morphology (with main focus on trichomes of leaves). Maximum likelihood (ML) and Bayesian Inference (BI) trees were inferred using the output of ipyrad which contained all the loci assembled into one super-matrix. Our phylogenetic reconstruction is consistent with the traditional division of this genus into two sections: Sect. *Platyptera* and Sect. *Pterocarya*. Furthermore, we have detected four types of trichomes in *Pterocarya*. The combined morphological and molecular data show: (1) that *P. macroptera* var. *delavayi* is very different from the other two varieties (var. *insignis* and var. *macroptera*) of this species, and thus indicating that *P. delavayi* probably merits a species status; and (2) that *P. tonkinensis* should be merged with *P. stenoptera*.

Poster presentation abstracts

Poster N°112

Different species or not different species? - study of the contact zone between mitochondrial lineages in the Grass snake *Natrix natrix*.

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Speciation is a complex process and classifying taxa currently under speciation in 'delimited' boxes is even more difficult. In order to determine the specific status, we analysed two contact zones between different mitochondrial lineages of the Grass snake *Natrix natrix* using portions of both nuclear and mitochondrial genomes.

On the one hand, a lack of gene flow was found at the contact zone along the Rhine region, even between individuals geographically separated by a few kilometres. Morphological differences were also present even a single parameter cannot differentiate individuals with high confidence. On the other hand, the eastern contact zone is wide, with a large nuclear admixture and overlap of the mitochondrial lineages.

Consequently, the Grass snake seems to present different stages of speciation and our study highlights the importance of contact zones to evaluate the specific status of taxa.

Poster presentation abstracts

Poster N°113

Barcoding failure in the *Pardosa lugubris* group: hybrid introgression caused by *Wolbachia*?

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Christian Kropf, Natural History Museum of Bern, University of Bern

Recently it was shown that CO1 barcoding does not recognise three closely related species of European wolf spiders, i. e. *Pardosa lugubris*, *P. saltans*, and *P. alacris*. Such failure of the barcoding approach may have different reasons; one of them concerns infections with endosymbiotic bacteria of the genus *Wolbachia* that occur in numerous terrestrial arthropods. These bacteria may use or mediate rare hybridisation events in their host species in order to spread across species boundaries. They are mediated via the egg cell and may homogenize the mitochondrial genome of two (or more) species. This has been shown in a few cases in Lepidoptera, Diptera and Hymenoptera. We tested 93 individuals of the three *Pardosa* species for *Wolbachia* infection. In only a single female of *P. lugubris* was the test positive. We conclude that infection with *Wolbachia* is probably not the reason for failure of the barcoding approach in the *Pardosa lugubris* group.

Poster presentation abstracts

Poster N°114

Conservation and restoration of Nardion grasslands in the Swiss northern Prealps

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Nora Rieder, University of Berne

Prof. Dr Raphaël Arlettaz, University of Berne

Dr Jean-Yves Humbert, University of Berne

Species-rich Nardion grasslands are high nature value habitats and under conservation concern in Switzerland. Despite the current protection measurements, the Bernese authorities noted a dichotomous degradation trend: either Nardion grasslands tended to be dominated by *Nardus stricta* or eutrophic plants, both leading to a disappearance of typical Nardion species. We investigated the underlying causes of this degradation process by assessing vegetation composition in 48 Nardion grasslands and linking it to soil, management and environmental variables. Orthopterans were also sampled.

The results show that Nardion grasslands managed by mowing (hay meadows) are rarely degraded compared to grazed Nardion grasslands (pastures). Within pastures, *N. stricta* cover is most problematic on north-exposed slopes and in summer pastures. Eutrophic plants are most abundant in small pastures with low soil Carbon/Nitrogen ratio indicating high nutrient availability. A plausible driver of both degradation trends is grazing intensity: at high grazing intensity, soil C/N ratio is low because of high dung deposition, thus the eutrophic species are dominant whereas at low grazing intensity *N. stricta* is dominant due to selective grazing. Both degradation trends show a negative impact on the orthopteran density, which gives further reason to protect species-rich Nardion grasslands. We propose to install temporarily fences that divide the pastures into smaller areas to homogenize grazing intensity.

Poster presentation abstracts

Poster N°115

Are early-life effects on social behaviour non-genetically inherited to the next generation?

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Developmental plasticity has pervasive effects on phenotypes, but the degree to which these effects carry over to future generations is largely unexplored. Cooperatively breeding cichlids, *Neolamprologus pulcher*, pursue one of two alternative life history trajectories depending on early social experience: dispersing early or staying in the natal group and help. We ask whether early life effects on the social behaviour of a parental generation can be non-genetically inherited to the offspring generation. In a 2x2 factorial design, we generated F0 breeder pairs that had been reared either with or without parents in early life. They produced F1 broods, half of which were reared with foster parents and half were reared without parents. This resulted in four lines, in which F1 fish either experienced the same (+F0/+F1 and -F0/-F1) or the opposite social environment as their parents (+F0/-F1 and -F0/+F1). Juvenile F1 were tested in an asymmetric competition test, in which a preassigned owner of a resource (stimulus fish) competed with a preassigned intruder (focal F1 fish) over access to the resource. All social behaviours were recorded. Based on previous work we predicted additive effects of the presence of parents in the F0 and the F1 generation on submissive behaviour. Results indicate effects of the F0 generation only. Contrary to prediction, this non-genetic inheritance affects aggressive behaviour. We discuss the implication of these results for the sociality in *N. pulcher*.

Poster presentation abstracts

Poster N°116

Handbook of protocols for standardized measurement of terrestrial invertebrate functional traits

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Trait-based approaches are increasingly being used to test mechanisms underlying species assemblages and biotic interactions across a wide range of organisms including terrestrial arthropods and to investigate resulting ecosystem processes. However, such an approach relies on the standardized measurement of functional traits that can be applied across taxa and regions. Currently, unified methods of trait measurements are lacking for terrestrial arthropods.

Early this year the first handbook of protocols for standardized measurement of terrestrial invertebrate functional traits has been published. It presents a comprehensive review and detailed protocol for a set of 28 traits known to be sensitive to global stressors and/or affecting ecosystem processes and services. The handbook gives recommendations how to measure these traits under standardized conditions across various terrestrial invertebrate taxonomic groups. It provides considerations and approaches that apply to almost all traits described, such as the selection of species and individuals needed for the measurements, the importance of intraspecific trait variability, how many populations or communities to sample and over which spatial scales.

The approaches outlined in the handbook provide a means to improve the reliability and predictive power of functional traits to explain community assembly, species diversity patterns, and ecosystem processes and services within and across taxa and trophic levels, allowing comparison of studies and running meta-analyses across regions and ecosystems. This handbook is only a first step towards standardizing trait methodology across the most studied terrestrial invertebrate groups, and the protocols are aimed to balance general applicability and requirements for special cases or particular taxa. Therefore, we envision this handbook as a common platform to which everyone is kindly invited to provide methodological input for additional special cases.

Poster presentation abstracts

Poster N°117

Food-web complexity alters the fitness landscape of an insect herbivore

Matthew Barbour, University of Zurich

Jordi Bascompte, University of Zurich

Studies of natural selection and fitness landscapes usually treat the network of interacting species as a “black box”. Given that the loss of biodiversity is simplifying the structure of ecological networks, there is a pressing need to answer the question: how does network complexity affect natural selection and the fitness landscape of associated species? To answer this question, we conducted a field experiment that manipulated the complexity of a food web associated with a galling insect herbivore. To maintain complex food webs, we allowed the entire community of natural enemies to attack insect galls on 64 plants in a common garden setting. To create simple food webs, we excluded a guild of three larval parasitoids by bagging galls on 64 different plants; therefore, mortality in this treatment was primarily due to a single egg parasitoid that attacks prior to gall formation. We then measured herbivore survival as a function of three key gall traits in each treatment. We found that more traits were under selection in the simple vs. complex food web. This occurred because different parasitoid species impose different selection pressures on gall traits, thereby minimizing relative fitness differences among insect galls with different phenotypes. Our work suggests that more complex food webs allow phenotypic variation to persist, which could facilitate subsequent adaptive evolution to environmental change.

Poster presentation abstracts

Poster N°118

Joint actions in humans and non-humans: A comparative framework to study shared intentionality

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Federico Rossano, University of California San Diego

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Humans are supposedly the only species capable of sharing intentions and goals during joint activities. This hypothesis is supported by evidence from experiments involving social games, during which only children, but not apes, were motivated to cooperate with human partners during collaborative tasks. However, these results have been questioned because apes were not tested with other apes, nor were they subjected to an ecologically relevant activity. To address these concerns, we present a new research programme to reassess the question of whether great apes are able of engaging in joint intentionality. To this end, we focus on how spontaneous social interaction with conspecifics are mutually constructed, maintained and terminated. We use a theoretical framework from developmental psychology by analysing joint actions as sequences of three distinct phases; opening, main body and closing, as well as the communication signals displayed by subjects to navigate between these phases. We argue that this framework allows for a systematic comparison of joint action coordination across animal species and human children. We will introduce our framework and illustrate it with empirical examples from social interactions of bonobos (*Pan paniscus*), e.g., social grooming. We discuss how our approach could shed light on the evolution of the peculiar human cognition-for-interaction.

Poster presentation abstracts

Poster N°119

Gene expression evolution in Lake Tanganyika cichlid fishes

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Walter Salzburger, University of Basel

Adaptive radiation is one of the most important evolutionary processes shaping the species diversity encountered on our planet. One striking example of adaptive radiation is found in Lake Tanganyika. The lake hosts hundreds of endemic species of cichlid fishes that have evolved in a few million years only and thus provide a unique system to study the molecular basis of speciation. And yet, it is not fully understood how intrinsic factors and external events interplay to promote this diversity. Gene expression regulation is a prime intrinsic factor and thought to be responsible for many phenotypic differences observed among the closely related cichlid species. To investigate the genomic landscape of speciation and the transcriptomal diversity of cichlids in this lake, we use a large scale analysis of gene expression evolution. To this end, we sequenced the transcriptomes of five tissues from dozens of representative of this large-scale adaptive radiation. By comparing gene expression patterns across the phylogenetic tree, we aim to identify candidate genes that could be involved in diversification. The comparative framework we conduct is so far the most thorough examination of the transcriptomal diversity of any adaptive radiation. By combining our expression data with already existing genomic and morphological data, we aspire to provide novel insights into cichlid speciation genomics and extend the current knowledge of how selection can act on an entire biological system.

Poster presentation abstracts

Poster N°120

Environmental drivers of community structure in the cichlid species flock of Lake Tanganyika

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The cichlid fishes in the East African Great Lake Tanganyika represent what is perhaps the most genetically, ecologically and morphologically diverse adaptive radiation on our planet. Detailed information on community structure and niche space is of great importance when attempting to understand the underlying mechanisms that led to such hyper-diverse species assemblages. Little attention, however, has so far been directed to the quantification of community structure in cichlids. This study strives to shed light on this neglected aspect of cichlid ecology and to assess the influence of environmental parameters on diversity and community structure. To this end, a series of Point-Combination Transects (PCT) with GoPro cameras were conducted in various locations and depths in Lake Tanganyika to capture its cichlid community. In contrast to the commonly applied UVC (Underwater Visual Census) methods, PCT provides an enhanced snapshot of an undisturbed community. The images represent the raw data of the study from which we assess the lake's cichlid community and diversity. 180 transects (resulting in over 300'000 images) have been conducted in Zambia and Tanzania since 2016. Results for Zambia indicate clear differentiation along two environmental axes, depth and rock coverage. Further analyses explored the correlation of these drivers on community structure. We seek to increase the knowledge of the Lake Tanganyika cichlid assemblage and the field of ecological speciation.

Poster presentation abstracts

Poster N°121

Comparing functions of copulation calls in wild olive baboons, *Papio anubis*, using multi-model inference

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Christof Neumann, University of Neuchâtel
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Female copulation calls are species-specific, distinct vocal signals sometimes given during or shortly after mating. Despite being common in primates and despite much empirical work, their function remains largely unclear for most species. Here, we used an information-theoretic approach to examine simultaneously three main competing hypotheses for the evolution of copulation calls. Two of the three hypotheses predict that female copulation calls function to incite competition between males, either directly (the male-male competition hypothesis) or indirectly (the sperm competition hypothesis), while the third one predicts that females use calls to choose mating partners (the female choice hypothesis). We collected data on copulations of wild female olive baboons to compare the relative support for these hypotheses by modelling whether or not females produced copulation calls after mounts. Our analytical approach enabled us to objectively rank models corresponding to the three hypotheses according to how well our data fit the models. Our data favoured the sperm competition hypothesis over the female choice hypotheses although much variation in calling remained unexplained. The male-male competition hypothesis seems unlikely given our data. We also discuss the possibility that copulation calls have no function, functions not included in our analysis, or that they are multifunctional, a reflection of the species social evolution history.

Flash talk abstracts

Poster N°122

Diversity and stability of rotifer-associated bacterial communities

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Rotifers are an important component of zooplankton in freshwater habitats. Their microbiome is still poorly investigated and its composition and function are not well understood. This project characterized freshwater rotifer microbiomes, by NGS of the 16S rDNA, to evaluate its variability between and within species and its adaptation to different environmental changes. The microbiomes of different rotifer species and those of the surrounding water were analysed and then compared with the microbiome of crustaceans from similar habitats. Moreover, rotifers were exposed to different food and temperatures to see if there were changes in their microbiome composition. The main result is that, in contrast to crustaceans, rotifers may not have a core microbiome. To support this finding, the number of Operational Taxonomic Units (OTUs) did not differ in the animals and in the surrounding water and the OTU composition of the diverse rotifers was very similar to those of the respective surrounding water. Despite many genera that are often host-associated genera (e.g. *Limnohabitans*) were found in rotifers, their abundance was very low (<1%). Furthermore, neither between species nor within species exposed to different conditions a real core microbiome of OTUs that were always present was found. As a conclusion, changes in food source rapidly changed the composition of rotifer microbiome.

Flash talk abstracts

Poster N°123

Causes and consequences of changes in bumblebee communities over time

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Gaëlle Beureux, University of Neuchatel
Giorgia Ferretti, University of Neuchatel
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Nils Arrigo, University of Lausanne
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Bumblebee communities in Switzerland have undergone significant changes in recent decades. Possible drivers of these changes include changes in floral resources due to modifications of agricultural practices, climate change, and interactions with pathogens. Here, we examine the evolution of bumblebee communities over time using all available Swiss data (60'000 observations collected between 1817 and 2017 for 42 species). Using distribution models and shifts in species frequency, we calculate an index of change in abundance (trends) for all species. We examine how several variables (phenology, tongue length, floral specialization, climatic preferences) predict trends. Lastly, we compare the historical genetic diversity of selected species with similar ecological niches but opposing trends. Results suggest significant associations between decline and phenology (late species have declined more than early species) and climatic niche (lowland, thermophilic species have declined more than high altitude, cold-adapted species). Species pairs with a similar niche but contrasting trends exhibited significant differences in genetic diversity (declining species had lower diversity than stable species). Our general conclusions are that climate change has so far had little impact on the drastic changes observed in communities and that the likely predominant driver of the decline is the reduced resource availability in late summer. The contribution of other factors is discussed.

Flash talk abstracts

Poster N°124

Improving small genome assemblies

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Juan I. Montoya-Burgos, University of Geneva - Dpt. of Genetics & Evolution

In recent years, sequencing technologies developments have enabled affordable whole-genome sequencing experiments and draft genomes are becoming ever more numerous. However, many have drawn the attention to the sometimes-questionable quality of these assemblies. Errors may often stem from multiple sources, but contamination of the biological material with unwanted DNA is too often overlooked.

Here, we introduce a novel approach combining sequence homology, base composition and sequencing coverage information to identify and remove possible contamination, both at the read (single-end and paired-end Illumina reads) and contig levels. Compared to other approaches tested, our method improved contiguation on a highly variable Archaeal genome (*Methanobrevibacter smithii*) by two orders of magnitude. Our pipeline is made available in a ready-to-use script.

Flash talk abstracts

Poster N°125

Exploring the HLA genetic diversity of the Mandenka population from Senegal

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The Human Leukocyte Antigen (HLA) is a highly variable genomic region encoding the major histocompatibility complex proteins involved in human immunity. With the aim to understand better which evolutionary forces shaped the HLA genetic diversity, we used Next Generation Sequencing (NGS) to analyse 8 HLA loci in a well-documented sub-Saharan African population. The detailed comparison of exons 2, 3, 4 and 5 nucleotide diversity at these loci reveals noteworthy differences among them: whereas most exons 2 and 3 are highly variable at non-synonymous sites, as expected from the function of their encoded regions to present pathogen-derived peptides to T lymphocytes, a lower diversity is found at HLA-C exon 3, whose encoded domain assumes a different role as KIR ligand; moreover, a peculiar diversity pattern is observed at HLA-A exon 2, which appears as a signature of the demographic history of the studied population. We also propose a molecular mechanism of gene conversion followed by a rapid selective sweep to explain the origin of the DRB1*13:04 allele and the high frequency of the DRB1*13:04~DQA1*05:05:01~DQB1*03:19 haplotype, likely protective to infection by *Onchocerca volvulus*, a prevalent pathogen in West Africa. This study shows the benefits of using NGS to decipher the molecular variation of HLA genes in relation to environmental pressures and demographic history, calling for complementary analyses on populations living in contrasting environments.

Flash talk abstracts

Poster N°126

Prediction of species occurrence by habitat network topology: Insights from Swiss Amphibians

Damian Ortiz Rodriguez, ETH Zürich / WSL Swiss Federal Research Institute

Maarten van Strien, ETH Zürich

Antoine Guisan, University of Lausanne

Adrienne Grêt-Regamey, ETH Zürich

Rolf Holderegger, WSL Swiss Federal Research Institute

Knowledge about the likely occurrence of species in specific habitat patches is of great importance for conservation and landscape planning, especially in fragmented landscapes under high human pressure. Predictive models addressing the determinants of the presence or absence of the species are needed to get such insights. These determinants include the quality of the habitat and the connectivity between the suitable patches. Another important – but underexplored – factor is the topological placement of the patches: their position in the overall architecture of the habitat network. We present results of a network-based model developed to predict the occurrence status of a species in all the patches of a habitat network, i.e., the network's occupancy-state configuration. Our focus species was the European tree frog (*Hyla arborea* L.) and its distribution in the densely populated Swiss Plateau. Our model is composed by of edges defined by cost surfaces and by nodes obtained from ensemble habitat suitability models, based on available species observation records. These nodes can have values of presence or absence, with the latter defined by sampling intensity thresholds. We compared the performance of logistic models that considered or excluded topological variables and found a significant correlation between the degree and the occupancy-state. The criteria of AIC and AUC also suggested that incorporating topological properties enhances the predictive power of the model.

Flash talk abstracts

Poster N°127

Species' range shifts drive the evolution of spatial difference in phenotypic plasticity and environmental tolerance

Max Schmid, University of Zurich

Ramon Dallo, ETH Zurich

Frédéric Guillaume, University of Zurich

Species exhibit remarkable abilities to inhabit a diverse set of environmental conditions, which manifests as environmental tolerance and has caught the interest of biologists early on. Recent empirical findings on ectotherms suggest that processes underlying changing species' ranges give rise to spatial differences in thermal tolerance within species. We used individual-based simulations to investigate how phenotypic plasticity and environmental tolerance evolve along shifting environmental gradients. We found that regions of a species' range which experienced a longer history or larger extent of environmental change generally exhibited increased plasticity or tolerance. Such regions may be at the trailing edge when a species is tracking its ecological niche in space (e.g., in a climate change scenario) or at the front edge when a species expands in a new habitat (e.g., in an expansion/invasion scenario). Overall, our findings highlight how variation in migration rates, rates of environmental change, and costs of plasticity affect the evolution of environmental tolerance and phenotypic plasticity.

Flash talk abstracts

Poster N°128

Surveying Mexican fields for biological control agents of the Western Corn Rootworm

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Carla Arce, University of Neuchâtel, Switzerland
Ricardo Machado, University of Bern, Switzerland
Angela Köhler, Hans Knöll Institute, Germany
Julio Bernal, Texas A&M University
Rebeca Alvarez Zagoya, Instituto Politécnico Nacional, Mexico
Juan Francisco Pérez-Domínguez, INIFAP México
Antonio Marín-Jarillo, INIFAP, México
Raquel Campos-Herrera, Universidade do Algarve, Portugal
Ted C. J. Turlings, University of Neuchâtel, Switzerland

The Western Corn Rootworm (WCR) *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), is a root-herbivore that specializes on maize (*Zea mays* L.). It is native to North America where it causes tremendous crop losses yearly, but also in parts of Europe where was recently introduced. Biological control strategies have been unsuccessful so far and there is an urgent need for more effective biocontrol agents. We screened for natural enemies of the root herbivore in Central Mexico, including parasitic flies, wasps and entomopathogenic nematodes (EPN). We examined adult beetles of the subtribe Diabroticina for the occurrence of the parasitoids *Celatoria compressa* Wulp (Diptera: Tachinidae) and *Centistes (Syrrhizus) diabroticae* Gahan (Hymenoptera: Braconidae), and we tested the virulence of the field-collected EPN against WCR larvae. This is a first step to obtain information and material for the development of an effective biocontrol agent against WCR.

Flash talk abstracts

Poster N°129

A quantitative framework to explore the dynamic of genomic landscapes in ecology and evolution

Claudio Sebastián Quilodrán Venegas, University of Oxford

Tim Coulson, University of Oxford

How organisms diverged into reproductively isolated species is a major question in evolution. The recent accumulation of genomic data provides promising opportunities to understand the genomic landscape of divergence, which describes the distribution of genomic differences across genomes. The genomic areas of unusually high differentiation have been called genomic islands of divergence. The main hypothesis to explain the appearance of these islands states they are areas related to divergent selection and resistant to gene flow. This pattern is thus associated with ecological or parapatric speciation. However, we currently lack a quantitative framework to describe the dynamic of genomic landscapes. Here, we propose an individual-based simulation framework to explore the dynamics of genomes with various scenarios of gene flow and selective pressures on single or multiple interacting gene networks. The simulations are focused either on theoretical or real genomes for which enough ecological and genetic information is available. We show that speciation with on-going gene flow is not the only route for the emergence of genomic islands. A similar pattern may also appear in allopatric conditions under the interactions between the architecture of target genomes, drift, and the adaptation to local environmental conditions. This framework represents a novel tool to explore quantitative expectations on the speciation process, useful to elucidate past and future evolution of any taxa.